

=> fil capl; d que 11

FILE 'CAPLUS' ENTERED AT 12:23:49 ON 23 FEB 2005
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
COPYRIGHT (C) 2005 AMERICAN CHEMICAL SOCIETY (ACS)

Copyright of the articles to which records in this database refer is held by the publishers listed in the PUBLISHER (PB) field (available for records published or updated in Chemical Abstracts after December 26, 1996), unless otherwise indicated in the original publications. The CA Lexicon is the copyrighted intellectual property of the American Chemical Society and is provided to assist you in searching databases on STN. Any dissemination, distribution, copying, or storing of this information, without the prior written consent of CAS, is strictly prohibited.

FILE COVERS 1907 - 23 Feb 2005 VOL 142 ISS 9
FILE LAST UPDATED: 22 Feb 2005 (20050222/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

'OBI' IS DEFAULT SEARCH FIELD FOR 'CAPLUS' FILE

L1 7 SEA FILE=CAPLUS ABB=ON KERMANI B?/AU

*inventor
search*

=> fil wpids; d que 148

FILE 'WPIDS' ENTERED AT 12:23:50 ON 23 FEB 2005
COPYRIGHT (C) 2005 THE THOMSON CORPORATION

FILE LAST UPDATED: 18 FEB 2005 <20050218/UP>
MOST RECENT DERWENT UPDATE: 200512 <200512/DW>
DERWENT WORLD PATENTS INDEX SUBSCRIBER FILE, COVERS 1963 TO DATE

>>> FOR A COPY OF THE DERWENT WORLD PATENTS INDEX STN USER GUIDE,
PLEASE VISIT:
http://www.stn-international.de/training_center/patents/stn_guide.pdf <<<

>>> FOR DETAILS OF THE PATENTS COVERED IN CURRENT UPDATES, SEE
<http://thomsonderwent.com/coverage/latestupdates/> <<<

>>> FOR INFORMATION ON ALL DERWENT WORLD PATENTS INDEX USER
GUIDES, PLEASE VISIT:
<http://thomsonderwent.com/support/userguides/> <<<

>>> NEW! FAST-ALERTING ACCESS TO NEWLY-PUBLISHED PATENT
DOCUMENTATION NOW AVAILABLE IN DERWENT WORLD PATENTS INDEX
FIRST VIEW - FILE WPIFV.
FOR FURTHER DETAILS: <http://www.thomsonderwent.com/dwpifv> <<<

>>> NEW DISPLAY FORMAT HITSTR ADDED ALLOWING DISPLAY OF
HIT STRUCTURES WITHIN THE BIBLIOGRAPHIC DOCUMENT <<<

>>> SMILES and ISOSMILES strings are no longer available as
Derwent Chemistry Resource display fields <<<

>>> THE CPI AND EPI MANUAL CODES HAVE BEEN REVISED FROM UPDATE 200501.
PLEASE CHECK:

<http://thomsonderwent.com/support/dwpioref/reftools/classification/code-revision/>
FOR DETAILS. <<<

L34 26 SEA FILE=WPIDS ABB=ON KERMANI B?/AU
L35 3564 SEA FILE=WPIDS ABB=ON ALLELE#
L36 2764 SEA FILE=WPIDS ABB=ON GENOTYP?
L37 156518 SEA FILE=WPIDS ABB=ON ARRAY#
L38 3468 SEA FILE=WPIDS ABB=ON MICROARRAY#
L39 15854 SEA FILE=WPIDS ABB=ON NORMALI?
L40 7980 SEA FILE=WPIDS ABB=ON (COORDINATE OR CO ORDINATE) (2A) SYSTEM#
L41 15 SEA FILE=WPIDS ABB=ON SWEEP POINT#
L42 3946 SEA FILE=WPIDS ABB=ON CONTROL POINT#
L43 581 SEA FILE=WPIDS ABB=ON (REGISTRATION OR CONFORMATION? OR
PROJECT?) (3A) TRANSFORM?
L44 31 SEA FILE=WPIDS ABB=ON DELAUNAY
L45 1584 SEA FILE=WPIDS ABB=ON TRIANGULAT?
L46 49 SEA FILE=WPIDS ABB=ON GENETIC DATA#
L47 4 SEA FILE=WPIDS ABB=ON L34 AND (L35 OR L36 OR L37 OR L38 OR
L39 OR L40 OR L41 OR L42 OR L43 OR L44 OR L45 OR L46)
L48 3 SEA FILE=WPIDS ABB=ON L47 NOT CLOCK#

=> fil JICST-EPLUS, PASCAL, BIOTECHNO, ESBIODBASE, BIOSIS, DISSABS, JAPIO, INSPEC,
COMPENDEX, COMPUSCIENCE, COMPUAB, SCISEARCH

FILE 'JICST-EPLUS' ENTERED AT 12:23:51 ON 23 FEB 2005
COPYRIGHT (C) 2005 Japan Science and Technology Agency (JST)

FILE 'PASCAL' ENTERED AT 12:23:51 ON 23 FEB 2005
Any reproduction or dissemination in part or in full,
by means of any process and on any support whatsoever
is prohibited without the prior written agreement of INIST-CNRS.
COPYRIGHT (C) 2005 INIST-CNRS. All rights reserved.

FILE 'BIOTECHNO' ENTERED AT 12:23:51 ON 23 FEB 2005
COPYRIGHT (C) 2005 Elsevier Science B.V., Amsterdam. All rights reserved.

FILE 'ESBIODBASE' ENTERED AT 12:23:51 ON 23 FEB 2005
COPYRIGHT (C) 2005 Elsevier Science B.V., Amsterdam. All rights reserved.

FILE 'BIOSIS' ENTERED AT 12:23:51 ON 23 FEB 2005
Copyright (c) 2005 The Thomson Corporation.

FILE 'DISSABS' ENTERED AT 12:23:51 ON 23 FEB 2005
COPYRIGHT (C) 2005 ProQuest Information and Learning Company; All Rights Reserved.

FILE 'JAPIO' ENTERED AT 12:23:51 ON 23 FEB 2005
COPYRIGHT (C) 2005 Japanese Patent Office (JPO)- JAPIO

FILE 'INSPEC' ENTERED AT 12:23:51 ON 23 FEB 2005
Compiled and produced by the IEE in association with FIZ KARLSRUHE
COPYRIGHT 2005 (c) INSTITUTION OF ELECTRICAL ENGINEERS (IEE)

FILE 'COMPENDEX' ENTERED AT 12:23:51 ON 23 FEB 2005
Compendex Compilation and Indexing (C) 2005
Elsevier Engineering Information Inc (EEI). All rights reserved.
Compendex (R) is a registered Trademark of Elsevier Engineering Information Inc.

FILE 'COMPUSCIENCE' ENTERED AT 12:23:51 ON 23 FEB 2005
COPYRIGHT (c) 2005 FACHINFORMATIONSZENTRUM KARLSRUHE (FIZ KARLSRUHE)

FILE 'COMPUAB' ENTERED AT 12:23:51 ON 23 FEB 2005
COPYRIGHT (C) 2005 Cambridge Scientific Abstracts (CSA)

FILE 'SCISEARCH' ENTERED AT 12:23:51 ON 23 FEB 2005
Copyright (c) 2005 The Thomson Corporation.

=> d que 174

L61 42 SEA KERMANI B?/AU
L62 315958 SEA ALLELE#
L63 367676 SEA GENOTYP?
L64 1845597 SEA GENETIC
L65 691272 SEA ARRAY#
L66 55463 SEA MICROARRAY#
L67 302708 SEA NORMALIZ? OR NORMALIS?
L68 41265 SEA (COORDINATE OR CO ORDINATE) (W) SYSTEM#
L69 19 SEA SWEEP POINT#
L70 16525 SEA CONTROL POINT#
L71 5953 SEA DELAUNAY
L72 30643 SEA TRIANGULAT?
L73 6608 SEA (REGIST? OR CONFORMATION? OR PROJECT?) (3A) TRANSFORM?
L74 23 SEA L61 AND (L62 OR L63 OR L64 OR L65 OR L66 OR L67 OR L68 OR
L69 OR L70 OR L71 OR L72 OR L73)

=> dup rem 11,174,148

FILE 'CAPLUS' ENTERED AT 12:23:54 ON 23 FEB 2005
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
COPYRIGHT (C) 2005 AMERICAN CHEMICAL SOCIETY (ACS)

FILE 'PASCAL' ENTERED AT 12:23:54 ON 23 FEB 2005
Any reproduction or dissemination in part or in full,
by means of any process and on any support whatsoever
is prohibited without the prior written agreement of INIST-CNRS.
COPYRIGHT (C) 2005 INIST-CNRS. All rights reserved.

FILE 'ESBIOBASE' ENTERED AT 12:23:54 ON 23 FEB 2005
COPYRIGHT (C) 2005 Elsevier Science B.V., Amsterdam. All rights reserved.

FILE 'BIOSIS' ENTERED AT 12:23:54 ON 23 FEB 2005
Copyright (c) 2005 The Thomson Corporation.

FILE 'DISSABS' ENTERED AT 12:23:54 ON 23 FEB 2005
COPYRIGHT (C) 2005 ProQuest Information and Learning Company; All Rights Reserved.

FILE 'INSPEC' ENTERED AT 12:23:54 ON 23 FEB 2005
Compiled and produced by the IEE in association with FIZ KARLSRUHE
COPYRIGHT 2005 (c) INSTITUTION OF ELECTRICAL ENGINEERS (IEE)

FILE 'COMPENDEX' ENTERED AT 12:23:54 ON 23 FEB 2005
Compendex Compilation and Indexing (C) 2005
Elsevier Engineering Information Inc (EEI). All rights reserved.
Compendex (R) is a registered Trademark of Elsevier Engineering Information Inc.

FILE 'COMPUAB' ENTERED AT 12:23:54 ON 23 FEB 2005
COPYRIGHT (C) 2005 Cambridge Scientific Abstracts (CSA)

FILE 'SCISEARCH' ENTERED AT 12:23:54 ON 23 FEB 2005
Copyright (c) 2005 The Thomson Corporation.

FILE 'WPIDS' ENTERED AT 12:23:54 ON 23 FEB 2005
COPYRIGHT (C) 2005 THE THOMSON CORPORATION
PROCESSING COMPLETED FOR L1
PROCESSING COMPLETED FOR L74
PROCESSING COMPLETED FOR L48

L91 18 DUP REM L1 L74 L48 (15 DUPLICATES REMOVED)
ANSWERS '1-7' FROM FILE CAPLUS
ANSWERS '8-10' FROM FILE PASCAL
ANSWERS '11-12' FROM FILE BIOSIS
ANSWER '13' FROM FILE DISSABS
ANSWER '14' FROM FILE INSPEC
ANSWER '15' FROM FILE COMPENDEX
ANSWER '16' FROM FILE COMPUAB
ANSWER '17' FROM FILE SCISEARCH
ANSWER '18' FROM FILE WPIDS

=> d ibib ed abs 1-7; d iall 8-18

L91 ANSWER 1 OF 18 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 1
ACCESSION NUMBER: 2004:398783 CAPLUS
DOCUMENT NUMBER: 141:100629
TITLE: Decoding randomly ordered DNA arrays
AUTHOR(S): Gunderson, Kevin L.; Kruglyak, Semyon; Graige, Michael S.; Garcia, Francisco; **Kermani, Bahram G.**; Zhao, Chanfeng; Che, Diping; Dickinson, Todd; Wickham, Eliza; Bierle, Jim; Doucet, Dennis; Milewski, Monika; Yang, Robert; Siegmund, Chris; Haas, Juergen; Zhou, Lixin; Oliphant, Arnold; Fan, Jian-Bing; Barnard, Steven; Chee, Mark S.
CORPORATE SOURCE: Illumina, Inc., San Diego, CA, 92121, USA
SOURCE: Genome Research (2004), 14(5), 870-877
CODEN: GEREFS; ISSN: 1088-9051
PUBLISHER: Cold Spring Harbor Laboratory Press
DOCUMENT TYPE: Journal
LANGUAGE: English

ED Entered STN: 17 May 2004

AB The authors have developed a simple and efficient algorithm to identify each member of a large collection of DNA-linked objects through the use of hybridization, and have applied it to the manufacture of randomly assembled arrays of beads in wells. Once the algorithm has been used to determine the identity of each bead, the microarray can be used in a wide variety of applications, including single nucleotide polymorphism genotyping and gene expression profiling. The algorithm requires only a few labels and several sequential hybridizations to identify thousands of different DNA sequences with great accuracy. The authors have decoded tens of thousands of arrays, each with 1520 sequences represented at .apprx.30-fold redundancy by up to .apprx.50,000 beads, with a median error rate of $<1 + 10^{-4}$ per bead. The approach makes use of error checking codes and provides, for the first time, a direct functional quality control of every element of each array that is manufactured. The algorithm can be applied to any spatially fixed collection of objects or mols. that are associated with specific DNA sequences.

REFERENCE COUNT: 50 THERE ARE 50 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L91 ANSWER 2 OF 18 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 2
ACCESSION NUMBER: 2003:654192 CAPLUS
TITLE: Automated information processing in randomly ordered arrays
INVENTOR(S): **Kermani, Bahram Ghaffarzadeh**; Haas, Juergen
PATENT ASSIGNEE(S): Illumina, Inc., USA

SOURCE: PCT Int. Appl.
 CODEN: PIXXD2
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 1
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003069333	A1	20030821	WO 2003-US4570	20030214
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				

PRIORITY APPLN. INFO.: US 2002-357213P P 20020214

ED Entered STN: 22 Aug 2003

AB The invention relates to the use of a computer system to compare images generated from a randomly ordered array. This system preserves the relative position of each site within the array so that the same site can be compared in different images.

REFERENCE COUNT: 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L91 ANSWER 3 OF 18 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 3

ACCESSION NUMBER: 2004:665013 CAPLUS

DOCUMENT NUMBER: 141:406396

TITLE: Highly parallel SNP genotyping

AUTHOR(S): Fan, J.-B.; Oliphant, A.; Shen, R.; Kermani, B.
 G.; Garcla, F.; Gunderson, K. L.; Hansen, M.;
 Steemers, F.; Butler, S. L.; Deloukas, P.; Galver, L.;
 Hunt, S.; McBride, C.; Bibikova, M.; Rubano, T.; Chen,
 J.; Wickham, E.; Doucet, D.; Chang, W.; Campbell, D.;
 Zhang, B.; Kruglyak, S.; Bentley, D.; Haas, J.;
 Rigault, P.; Zhou, L.; Stuelpnagel, J.; Chee, M. S.

CORPORATE SOURCE: Illumina, Inc., San Diego, CA, 92121, USA

SOURCE: Cold Spring Harbor Symposia on Quantitative Biology
 (2003), 68, 69-78

CODEN: CSHSAZ; ISSN: 0091-7451

PUBLISHER: Cold Spring Harbor Laboratory Press

DOCUMENT TYPE: Journal

LANGUAGE: English

ED Entered STN: 16 Aug 2004

AB A flexible, accurate, and scalable genotyping system, and have achieved high accuracy together with high call rates was developed. Conventional wisdom was that single-plex assays would be more accurate than highly multiplexed assay, and that it would be difficult to optimize assays in a multiplex format. In fact, the accuracy and call rates are similar to those obtained from single-plex genotyping systems, but at over 1,000 times the assay sequence complexity. These results demonstrate the specificity of the GoldenGate assay format, as well as the reproducibility and accuracy of the BeadArray platform and the BeadLab genotyping system as a whole. The Goldengate assay format is an exemplar for a new class of highly multiplexed assays that utilize parallel read about systems. It represents a significant departure from single and low-multiplex assays and is well suited for large-scale anal. of complex biol. systems.

REFERENCE COUNT: 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS

RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L91 ANSWER 4 OF 18 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 4
 ACCESSION NUMBER: 2002:123361 CAPLUS
 DOCUMENT NUMBER: 136:147506
 TITLE: Automated information processing in randomly ordered arrays
 INVENTOR(S): Stuelpnagel, John A.; Chee, Mark; Dickinson, Todd A.; Gunderson, Kevin; **Kermani, Bahram G.**
 PATENT ASSIGNEE(S): Illumina, Inc., USA
 SOURCE: PCT Int. Appl., 56 pp.
 CODEN: PIXXD2
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 3
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002012897	A2	20020214	WO 2001-US24882	20010809
WO 2002012897	C2	20030403		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
CA 2419058	AA	20020214	CA 2001-2419058	20010809
AU 2001084760	A5	20020218	AU 2001-84760	20010809
PRIORITY APPLN. INFO.:			US 2000-636387	A 20000809
			WO 2001-US24882	W 20010809

ED Entered STN: 15 Feb 2002

AB The invention relates to the use of a computer system to compare images generated from a randomly ordered array. This system preserves the relative position of each site within the array so that the same site can be compared in different images.

L91 ANSWER 5 OF 18 CAPLUS COPYRIGHT 2005 ACS on STN
 ACCESSION NUMBER: 2002:794199 CAPLUS
 DOCUMENT NUMBER: 137:259628
 TITLE: Automated information processing in randomly ordered arrays
 INVENTOR(S): Stuelpnagel, John R.; Chee, Mark S.; Dickinson, Todd A.; **Kermani, Bahram G.**; Haas, Juergen
 PATENT ASSIGNEE(S): USA
 SOURCE: U.S. Pat. Appl. Publ., 28 pp., Cont.-in-part of U.S. Ser. No. 636,387.
 CODEN: USXXCO
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 3
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2002150909	A1	20021017	US 2001-925941	20010809
PRIORITY APPLN. INFO.:			US 1999-119323P	P 19990209
			US 2000-500555	A2 20000209

US 2000-636387

A2 20000809

ED Entered STN: 18 Oct 2002

AB The invention relates to the use of a computer system to compare images generated from a randomly ordered array. This system preserves the relative position of each site within the array so that the same site can be compared in different images.

L91 ANSWER 6 OF 18 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2001:521036 CAPLUS
TITLE: Multi-dimensional optical disk
INVENTOR(S): **Kermani, Bahram Ghaffarzadeh**
PATENT ASSIGNEE(S): Lucent Technologies Inc., USA
SOURCE: Eur. Pat. Appl.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 1117093	A2	20010718	EP 2000-311059	20001212
EP 1117093	A3	20021127		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
US 6826143	B1	20041130	US 2000-482960	20000114
PRIORITY APPLN. INFO.:			US 2000-482960	A 20000114

ED Entered STN: 19 Jul 2001

AB The present invention provides an optical disk with pits and/or bumps which each contain a plurality of facets. Each facet of each pit and/or bump is intended for sep. read back as an individual 'side' of the optical disk (much as vinyl records had two 'sides' for sep. playback). The sep. 'sides' of the optical disk formed by sep. facets of each pit and/or bump can be read back either simultaneously or serially, either by a corresponding plurality of laser beams, or by a common laser beam which is positioned to a first orientation with respect to a rotating track to focus on a first set of facets of each pit and/or bump, and then repositioned to focus on a second set of facets of the same set of pits and/or bumps and thus to read a second 'side' of the optical disk. The technique may be extended to provide a single optical disk and even a single track of the optical disk with even more than two 'sides' by using three-, four- or five-sided pyramidal-shaped pits and/or bumps.

L91 ANSWER 7 OF 18 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2000:830504 CAPLUS
TITLE: Integrated circuit having reduced probability of wire-bond failure
INVENTOR(S): **Kermani, Bahram Ghaffarzadeh**
PATENT ASSIGNEE(S): Lucent Technologies Inc., USA
SOURCE: U.S., 9 pp.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 6153506	A	20001128	US 1999-263075	19990308
PRIORITY APPLN. INFO.:			US 1999-263075	19990308

ED Entered STN: 28 Nov 2000

AB The present invention provides an improved integrated circuit technique

for increasing the reliability of wire-bonds in an integrated circuit by increasing the contact angle between certain pins and their respective wire-bonds, particularly those pins otherwise most susceptible to wire-bond failure, i.e., those pins conventionally located toward the corners of a conventional integrated circuit. By doing so, the overall length of the wire-bonds in a chip will be reduced, which in turn can result in further reduction of the probability of wire-bond failures. In a disclosed embodiment, a five or more sided integrated circuit shape is introduced wherein pads on up to four sides of an integrated circuit wafer chip are bonded to pins supported on eight edges of an integrated circuit package. An integrated circuit having at least five pin-supporting edges renders more robust wire-bond angles for any given integrated circuit package size.

REFERENCE COUNT: 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L91 ANSWER 8 OF 18 PASCAL COPYRIGHT 2005 INIST-CNRS. ALL RIGHTS RESERVED.
on STN DUPLICATE 6

ACCESSION NUMBER: 1999-0203912 PASCAL

COPYRIGHT NOTICE: Copyright .COPYRG. 1999 INIST-CNRS. All rights reserved.

TITLE (IN ENGLISH): Using neural networks and **genetic** algorithms to enhance performance in an electronic nose

AUTHOR: **KERMANI B. G.**; SCHIFFMAN S. S.; NAGLE H. T.

CORPORATE SOURCE: Lucent Technologies, Allentown, PA 18103, United States; Department of Psychiatry, Duke University Medical Center, Durham, NC 27710-2159, United States; Department of Electrical and Computer Engineering, North Carolina State University, Raleigh, NC 27695-7911, United States

SOURCE: IEEE transactions on biomedical engineering, (1999), 46(4), 429-439, 49 refs.

ISSN: 0018-9294 CODEN: IEBEAX

DOCUMENT TYPE: Journal

BIBLIOGRAPHIC LEVEL: Analytic

COUNTRY: United States

LANGUAGE: English

AVAILABILITY: INIST-222E5, 354000074863020080

ABSTRACT: Sensitivity, repeatability, and discernment are three major issues in any classification problem. In this study, an electronic nose with an **array** of 32 sensors was used to classify a range of odorous substances. The collective time response of the sensor **array** was first partitioned into four time segments, using four smooth time-windowing functions. The dimension of the data associated with each time segment was then reduced by applying the Karhunen-Loeve (truncated) expansion (KLE). An ensemble of the reduced data patterns was then used to train a neural network (NN) using the Levenberg-Marquardt (LM) learning method. A **genetic** algorithm (GA)-based evolutionary computation method was used to devise the appropriate NN training parameters, as well as the effective database partitions/features. Finally, it was shown that a GA-supervised NN system (GANN) outperforms the NN-only classifier, for the classes of the odorants investigated in this study (fragrances, hog farm air, and soft beverages).

CLASSIFICATION CODE: 001D02C07; Applied sciences; Artificial intelligence
CONTROLLED TERM: Neural network; Improvement; Performance evaluation;
Genetic algorithm; Sensitivity analysis;
Reproducibility; Electronic nose; Artificial
intelligence; System response; Olfactometry
BROADER TERM: Biomedical data processing

L91 ANSWER 9 OF 18 PASCAL COPYRIGHT 2005 INIST-CNRS. ALL RIGHTS RESERVED.
on STN DUPLICATE 7

ACCESSION NUMBER: 2000-0146035 PASCAL
TITLE (IN ENGLISH): Novel method for reducing the dimensionality in a
sensor **array**
AUTHOR: **KERMANI B. G.**; SCHIFFMAN S. S.; NAGLE H. T.
CORPORATE SOURCE: North Carolina State Univ, Raleigh NC, United States
SOURCE: IEEE Transactions on Instrumentation and Measurement,
(1998), 47(3), 728-741, 18 refs.
ISSN: 0018-9456 CODEN: IEIMAO
DOCUMENT TYPE: Journal
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: United States
LANGUAGE: English
AVAILABILITY: INIST-222 G1
ABSTRACT: Specific types of gas sensors are normally produced by
adding different dopants to a common substrate. The
advancement of technology has made the fabrication of
many dopants and consequently various sensors
possible. As a result, in each family of gas sensors,
one can find tens of different sensors which are only
slightly different in the spectrum of response to
various volatile compounds. The wide variety of
available gas sensors creates a selection problem for
any specific application. Sensor selection/reduction
becomes even more important when cost and technology
limitations are issues of concern. Accordingly, a
methodology by which one can tailor a sensor
array to a specific need is highly desirable.
In this paper, a novel method is introduced to address
this task using data from an electronic nose that uses
polymer gas sensors. This method has been delineated
based on the geometry of eigenvectors in
Karhunen-Loeve expansion. The methodology is general
and therefore suitable for many other feature
selection problems.

CLASSIFICATION CODE: 001C01; Chemistry; General chemistry, Physical
chemistry
001D02B07B; Applied sciences; Computer science,
Software
001D02C; Applied sciences; Artificial intelligence
CONTROLLED TERM: Electronic nose; Karhunen-Loeve expansion; Theory;
Sensor data fusion; Data compression; Neural networks;
Odors; Chemical sensors

L91 ANSWER 10 OF 18 PASCAL COPYRIGHT 2005 INIST-CNRS. ALL RIGHTS RESERVED.
on STN DUPLICATE 8

ACCESSION NUMBER: 1997-0286825 PASCAL
COPYRIGHT NOTICE: Copyright .COPYRGT. 1997 INIST-CNRS. All rights
reserved.
TITLE (IN ENGLISH): Analysis of medication off-odors using an electronic
nose
AUTHOR: SCHIFFMAN S. S.; **KERMANI B. G.**; NAGLE H. T.
CORPORATE SOURCE: Department of Psychiatry, Box 3259, Duke University
Medical Center, Durham, NC 27710, United States;

Department of Electrical and Computer Engineering,
North Carolina State University, Raleigh, NC 27695,
United States

SOURCE: Chemical senses, (1997), 22(2), 119-128, refs. 1p. 1/4
ISSN: 0379-864X CODEN: CHSED8

DOCUMENT TYPE: Journal

BIBLIOGRAPHIC LEVEL: Analytic

COUNTRY: United Kingdom

LANGUAGE: English

AVAILABILITY: INIST-16455, 354000065253160020

ABSTRACT: Packaging materials have been implicated as a source for off-odors in pharmaceutical products. A new instrumentation method employing an **array** of conducting polymer gas sensors was used to identify the offending packaging components in the canister of a pharmaceutical inhalant. A case study is described in which tainted inhalers as well as elastomeric components of the canisters were 'sniffed' by the electronic nose. The electronic nose was able to differentiate between tainted and untainted canisters. Signal processing algorithms performed on the raw data from the sensors suggested that specific elastomeric components were responsible for the off-odor. A further experiment suggested that the propellant (Freon) extracted the odor from the elastomeric components as the medication was expelled from the canister. These data indicate that the electronic nose is a potential tool to solve odor problems in which human odor assessment is not feasible due to excess exposure to the medically active ingredient.

CLASSIFICATION CODE: 002B02A03; Life sciences; Medical sciences; Pharmacology

CONTROLLED TERM: Package; Odor; Defect; Measurement method; Instrumentation; Elastomer; Human

BROADER TERM: Perception; Methodology

L91 ANSWER 11 OF 18 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation. on
STN DUPLICATE 5

ACCESSION NUMBER: 2001:558820 BIOSIS

DOCUMENT NUMBER: PREV200100558820

TITLE: Randomly assembled **arrays** for SNP **genotyping**.

AUTHOR(S): Chee, M. [Reprint author]; Fan, J.-B. [Reprint author]; Wenz, M.; Wickham, E. [Reprint author]; Hayashibara, K.; Chen, J. [Reprint author]; Paner, T.; Doucet, D. [Reprint author]; Zhou, L. [Reprint author]; **Kermani, B.** [Reprint author]; Shen, R. [Reprint author]; Hansen, M. [Reprint author]; Steemers, F. [Reprint author]; Zhao, C. [Reprint author]; Barnard, S. [Reprint author]; Che, D. [Reprint author]; Gunderson, K. [Reprint author]; Barker, D. [Reprint author]; Efcavitch, J.; Oliphant, A. [Reprint author]

CORPORATE SOURCE: Illumina, Inc., San Diego, CA, USA

SOURCE: American Journal of Human Genetics, (October, 2001) Vol. 69, No. 4 Supplement, pp. 516. print.
Meeting Info.: 51st Annual Meeting of the American Society of Human Genetics. San Diego, California, USA. October 12-16, 2001.
CODEN: AJHGAG. ISSN: 0002-9297.

DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
Conference; (Meeting Poster)

LANGUAGE: English
ENTRY DATE: Entered STN: 5 Dec 2001
Last Updated on STN: 25 Feb 2002
CONCEPT CODE: General biology - Symposia, transactions and proceedings
00520
Genetics - General 03502
Biochemistry studies - General 10060
Biochemistry studies - Nucleic acids, purines and
pyrimidines 10062
INDEX TERMS: Major Concepts
Biochemistry and Molecular Biophysics; Genetics; Methods
and Techniques
INDEX TERMS: Chemicals & Biochemicals
oligonucleotide
INDEX TERMS: Methods & Equipment
SNP **genotyping** [single nucleotide polymorphism
genotyping]: **genetic** method
INDEX TERMS: Miscellaneous Descriptors
Meeting Abstract; Meeting Poster

L91 ANSWER 12 OF 18 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation. on
STN

ACCESSION NUMBER: 2002:616036 BIOSIS
DOCUMENT NUMBER: PREV200200616036
TITLE: A SNP linkage panel **genotyped** at approx 1,000-plex
on randomly assembled **arrays**.
AUTHOR(S): Hansen, M. S. T. [Reprint author]; Oliphant, A. [Reprint
author]; Fan, J.-B. [Reprint author]; Shen, R. [Reprint
author]; Zhou, L. [Reprint author]; **Kermani, B.**
[Reprint author]; Kruglyak, S. [Reprint author]; Dickinson,
T. [Reprint author]; Zhao, C. [Reprint author]; Barnard, S.
[Reprint author]; Che, D. [Reprint author]; Gunderson, K.
[Reprint author]; Barker, D. [Reprint author]; Chee, M. S.
[Reprint author]
CORPORATE SOURCE: Illumina, Inc., San Diego, CA, USA
SOURCE: American Journal of Human Genetics, (October, 2002) Vol.
71, No. 4 Supplement, pp. 204. print.
Meeting Info.: 52nd Annual Meeting of the American Society
of Human Genetics. Baltimore, MD, USA. October 15-19, 2002.
American Society of Human Genetics.
CODEN: AJHGAG. ISSN: 0002-9297.
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)

LANGUAGE: English
ENTRY DATE: Entered STN: 4 Dec 2002
Last Updated on STN: 4 Dec 2002
CONCEPT CODE: General biology - Symposia, transactions and proceedings
00520
Genetics - General 03502
INDEX TERMS: Major Concepts
Genetics; Methods and Techniques
INDEX TERMS: Methods & Equipment
single nucleotide polymorphism assay: **genetic**
method
INDEX TERMS: Miscellaneous Descriptors
genetic map; **genotyping**; physical
map; single nucleotide polymorphism panel; Meeting
Abstract

L91 ANSWER 13 OF 18 DISSABS COPYRIGHT (C) 2005 ProQuest Information and
Learning Company; All Rights Reserved on STN
ACCESSION NUMBER: 96:52587 DISSABS Order Number: AAR9627637

TITLE: ON USING ARTIFICIAL NEURAL NETWORKS AND **GENETIC**
ALGORITHMS TO OPTIMIZE PERFORMANCE OF AN ELECTRIC NOSE
(OLFACTORY)

AUTHOR: **KERMANI, BAHRAM GHAFARZADEH [PH.D.]**; NAGLE, H.
TROY [advisor]

CORPORATE SOURCE: NORTH CAROLINA STATE UNIVERSITY (0155)

SOURCE: Dissertation Abstracts International, (1996) Vol. 57, No.
4B, p. 2754. Order No.: AAR9627637. 213 pages.

DOCUMENT TYPE: Dissertation

FILE SEGMENT: DAI

LANGUAGE: English

ENTRY DATE: Entered STN: 19960903
Last Updated on STN: 19960903

ABSTRACT: In recent years, researchers have tried to mimic the
human nose using an **array** of gas sensors in a
computer-controlled instrument called the electronic nose
(Bartlett and Ling-Chung, 1989; Shurmer et al., 1990b;
Chandler and Pletcher, 1985; Gardner et al., 1991b; Heinze,
1990; Miasik et al., 1986; Persaud, 1991; Stetter et al.,
1986; Zaromb and Stetter, 1985; Cranny and Atkinson, 1992).
Commercial electronic nose systems (AromaScan, 1994;
Neotronics, 1994; Alpha MOS, 1994) use **arrays** of
gas sensors, with wide sensitivities, to differentiate
between various odorants. This differentiation is based on
the uniqueness of the data fingerprints of each odorant. A
data fingerprint is the accumulative processed response of
the **array** of gas sensors. In order to achieve a
high recognition rate, it is of paramount importance that
the odorprints (fingerprints) be unique and repeatable for
each odorant substance. In practice, it has been shown that
this uniqueness and repeatability of the data odorprints
are difficult to achieve. In reality, the experiments have
shown that, for odorants with a small number of volatile
molecules such as soft beverages, the current
state-of-the-art gas sensor species do not provide useful
odorprints. This fact is demonstrated for conducting
polymer sensors, which were used in this study. Therefore,
a complex signal processing and pattern recognition
methodology is needed to overcome the deficit in sensor
technology. In this investigation, artificial neural
networks have been employed, in conjunction with
genetic algorithms and traditional signal
processing techniques, to perform pattern recognition and
data classification. In an attempt to extract more
information from the sensor responses, the transient time
response of sensors has been used as well as their
steady-state values. Several case studies have been
performed on a diverse set of families of odorant sources,
e.g., coffees, perfumes, soda beverages and hog farm
samples. The case studies exhibit promising results in the
classification of various substances within each family of
odorants. Sophisticated signal processing methods have been
shown to be capable of compensating for the deficits in
sensor technology.

CLASSIFICATION: 0544 ENGINEERING, ELECTRONICS AND ELECTRICAL; 0541
ENGINEERING, BIOMEDICAL; 0800 ARTIFICIAL INTELLIGENCE

L91 ANSWER 14 OF 18 INSPEC (C) 2005 IEE on STN

ACCESSION NUMBER: 1997:5657282 INSPEC

DOCUMENT NUMBER: A9718-8760J-021; B9709-7510B-250; C9709-7330-269

TITLE: Feature extraction by **genetic** algorithms for
neural networks in breast cancer classification.

AUTHOR: Kermani, B.G.; White, M.W.; Nagle, H.T.
(Dept. of Electr. & Comput. Eng., North Carolina State Univ., Raleigh, NC, USA)

SOURCE: 1995 IEEE Engineering in Medicine and Biology 17th Annual Conference and 21 Canadian Medical and Biological Engineering Conference (Cat. No.95CH35746)
New York, NY, USA: IEEE, 1997. p.831-2 vol.1 of 2 vol. ixviii+1738 pp. 8 refs.
Conference: Montreal, Que., Canada, 20-23 Sept 1995
Price: CCCC 0 7803 2475 7/97/\$10.00
ISBN: 0-7803-2475-7

DOCUMENT TYPE: Conference Article

TREATMENT CODE: Practical

COUNTRY: United States

LANGUAGE: English

ABSTRACT: In today's world, in which computerized recognition is expanding its horizons in the field of medicine, breast cancer classification is receiving wide attention. In this application, artificial neural networks have achieved reasonable recognition rates. However, to improve performance, a technique is needed to screen the features of the input data, to extract the important ones and suppress those that are irrelevant. Although neural networks do have this capability to some extent, here it is shown that by using a hybrid **genetic** algorithm and neural network (GANN), the feature extraction can be performed more effectively. Another advantage of augmenting NN training with a GA is that the extracted features using GA are explicit and perceivable. Although the authors evaluated the technique using breast cancer data, the methodology is designed to handle any other kind of classification task.

CLASSIFICATION CODE: A8760J X-rays and particle beams (medical uses); A8770E Patient diagnostic methods and instrumentation; B7510B Radiation and radioactivity applications in biomedicine; B6140C Optical information, image and video signal processing; C7330 Biology and medical computing; C5290 Neural computing techniques; C5260B Computer vision and image processing techniques

CONTROLLED TERM: DIAGNOSTIC RADIOGRAPHY; FEATURE EXTRACTION; **GENETIC** ALGORITHMS; IMAGE CLASSIFICATION; MEDICAL IMAGE PROCESSING; NEURAL NETS

SUPPLEMENTARY TERM: **genetic algorithm feature extraction**; breast cancer classification; computerized recognition; input data features screening; **hybrid genetic algorithm**; important data extraction; irrelevant data suppression; X-ray images; medical diagnostic imaging

ELEMENT TERM: In

L91 ANSWER 15 OF 18 COMPENDEX COPYRIGHT 2005 EEI on STN

ACCESSION NUMBER: 1997(20):4137 COMPENDEX

TITLE: Feature extraction by **genetic** algorithms for neural networks in breast cancer classification.

AUTHOR: Kermani, Bahram G. (North Carolina State Univ, Raleigh, NC, USA); White, Mark W.; Nagle, H.Troy

MEETING TITLE: Proceedings of the 1995 IEEE Engineering in Medicine and Biology 17th Annual Conference and 21st Canadian Medical and Biological Engineering Conference.

MEETING ORGANIZER: IEEE

MEETING LOCATION: Montreal, Can

MEETING DATE: 20 Sep 1995-23 Sep 1995
SOURCE: Annual International Conference of the IEEE
Engineering in Medicine and Biology - Proceedings v 17
n 1 1995., 95CB35746.p 831-832
CODEN: CEMBAD ISSN: 0589-1019
PUBLICATION YEAR: 1995
MEETING NUMBER: 46181
DOCUMENT TYPE: Conference Article
TREATMENT CODE: Application
LANGUAGE: English
ABSTRACT: In today's world, in which computerized recognition is
expanding its horizons in the field of medicine,
breast cancer classification is receiving wide
attention. In this application, artificial neural
networks have achieved reasonable recognition rates
left bracket 1,2 right bracket .However, to improve
performance, a technique is needed to screen the
features of the input data, to extract the important
ones and suppress those that are irrelevant. Although
neural networks do have this capability to some
extent, in this paper it is shown that by using a
hybrid **Genetic** Algorithm and Neural Network
(GANN), the feature extraction can be performed more
effectively. Another advantage of augmenting NN
training with a GA is that the extracted features
using GA are explicit and perceivable. Although we
evaluated the technique using breast cancer data left
bracket 3 right bracket , the methodology is designed
to handle any other kind of classification
task.(Author abstract) 8 Refs.

CLASSIFICATION CODE: 723.4 Artificial Intelligence; 461.2 Biological

CONTROLLED TERM: Materials; 723.2 Data Processing
*Neural networks; Oncogenic viruses; Feature
extraction; Performance; Backpropagation;
Genetic algorithms; Pattern recognition

SUPPLEMENTARY TERM: Breast cancer classification; Breast cancer; Radial
basis; Feature selection

L91 ANSWER 16 OF 18 COMPUAB COPYRIGHT 2005 Cambridge Scientific Abstracts
on STN

ACCESSION NUMBER: 1999:5664 COMPUAB

DOCUMENT NUMBER: 395584 (CI)

TITLE: Using neural networks and **genetic** algorithms to
enhance performance in an electronic nose

AUTHOR: **Kermani B G**; Schiffman S S; Nagle H T

CORPORATE SOURCE: Lucent Technologies, Allentown, PA, USA.

SOURCE: IEEE Transactions on Biomedical Engineering, Vol. 46, No. 4
, pp. 429-439, 19990000. Publisher: Institute of Electrical
and Electronics Engineers, Inc , 445Hoes Ln, Piscataway,
NJ, 08854-1331, UK, [mailto:inspec@ieee.org].
ISSN: 0018-9294.

DOCUMENT TYPE: Journal

FILE SEGMENT: Computer & Information Systems

LANGUAGE: English

ENTRY DATE: Entered STN: 20041219

Last Updated on STN: 20041219

ABSTRACT: Sensitivity, repeatability, and discernment are three major
issues in any classification problem. In this study, an
electronic nose with an **array** of 32 sensors was
used to classify a range of odorous substances. The
collective time response of the sensor **array** was
first partitioned into four time segments, using four

smooth time-windowing functions. The dimension of the data associated with each time segment was then reduced by applying the Karhunen-Loeve (truncated) expansion (KLE). An ensemble of the reduced data patterns was then used to train a neural network (NN) using the Levenberg-Marquardt (LM) learning method. A **genetic** algorithm (GA)-based evolutionary computation method was used to devise the appropriate NN training parameters, as well as the effective database partitions/features. Finally, it was shown that a GA-supervised NN system (GANN) outperforms the NN-only classifier, for the classes of the odorants investigated in this study (fragrances, hog farm air, and soft beverages).

CLASSIFICATION: W4 723.4 Artificial Intelligence; C 723.4 Artificial Intelligence; W4 461.4 Human Engineering; W4 723.5 Computer Applications; W4 723.2 Data Processing; C 461.4 Human Engineering; C 723.5 Computer Applications; C 723.2 Data Processing (CI)

UNCONTROLLED TERM: **Genetic** Algorithms; Sensory Perception; Artificial Intelligence; Pattern Recognition; Digital Signal Processing

L91 ANSWER 17 OF 18 SCISEARCH COPYRIGHT (c) 2005 The Thomson Corporation.
on STN

ACCESSION NUMBER: 2003:347429 SCISEARCH
THE GENUINE ARTICLE: 594AC
TITLE: A SNP linkage panel **genotyped** at similar to 1,000-plex on randomly assembled **arrays**.
AUTHOR: Hansen M S T (Reprint); Oliphant A; Fan J B; Shen R; Zhou L; **Kermani** B; Kruglyak S; Dickinson T; Zhao C; Barnard S; Che D; Gunderson K; Barker D; Chee M S
CORPORATE SOURCE: Illumina Inc, San Diego, CA USA
COUNTRY OF AUTHOR: USA
SOURCE: AMERICAN JOURNAL OF HUMAN GENETICS, (OCT 2002) Vol. 71, No. 4, Supp. [S], pp. 204-204. MA 203.
Publisher: UNIV CHICAGO PRESS, 1427 E 60TH ST, CHICAGO, IL 60637-2954 USA.
ISSN: 0002-9297.
DOCUMENT TYPE: Conference; Journal
LANGUAGE: English
REFERENCE COUNT: 0
CATEGORY: GENETICS & HEREDITY

L91 ANSWER 18 OF 18 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
ACCESSION NUMBER: 2000-533047 [48] WPIDS
CROSS REFERENCE: 2002-196268 [25]
DOC. NO. NON-CPI: N2000-394270
DOC. NO. CPI: C2000-158878
TITLE: **Array** of microspheres, useful e.g. for detecting specific analytes, includes fiducial components to allow computerized comparison of data images from the **array**.
DERWENT CLASS: B04 D16 J04 S03
INVENTOR(S): BREZNER, D J; CHEE, M S; DICKINSON, T A; GUNDERSON, K; STUELPNAGEL, J R; HAAS, J; **KERMANI, B G**
PATENT ASSIGNEE(S): (ILLU-N) ILLUMINA INC; (CHEE-I) CHEE M S; (DICK-I) DICKINSON T A; (HAAS-I) HAAS J; (KERM-I) KERMANI B G; (STUE-I) STUELPNAGEL J R
COUNTRY COUNT: 90
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG	MAIN	IPC
-----------	------	------	------	----	----	------	-----

```

-----
WO 2000047996 A2 20000817 (200048)* EN 49 G01N033-50
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL
   OA PT SD SE SL SZ TZ UG ZW
W: AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CR CU CZ DE DK DM EE ES
   FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS
   LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ
   TM TR TT TZ UA UG UZ VN YU ZA ZW
AU 2000033594 A 20000829 (200062) G01N033-50
EP 1206315 A2 20020522 (200241) EN B01J019-00
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT
   RO SE SI
US 2002150909 A1 20021017 (200270) C12Q001-68
JP 2002536665 W 20021029 (200274) 71 G01N033-53
AU 771458 B2 20040325 (200454) G01N033-50
CA 2359352 C 20040921 (200463) EN B01J019-00
AU 2004202799 A1 20040722 (200471)# G01N033-50

```

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2000047996	A2	WO 2000-US3375	20000209
AU 2000033594	A	AU 2000-33594	20000209
EP 1206315	A2	EP 2000-911745	20000209
		WO 2000-US3375	20000209
US 2002150909	A1 Provisional	US 1999-119323P	19990209
	CIP of	US 2000-500555	20000209
	CIP of	US 2000-636387	20000809
		US 2001-925941	20010809
JP 2002536665	W	JP 2000-598854	20000209
		WO 2000-US3375	20000209
AU 771458	B2	AU 2000-33594	20000209
CA 2359352	C	CA 2000-2359352	20000209
		WO 2000-US3375	20000209
AU 2004202799	A1	AU 2004-202799	20040623

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 2000033594	A Based on	WO 2000047996
EP 1206315	A2 Based on	WO 2000047996
JP 2002536665	W Based on	WO 2000047996
AU 771458	B2 Previous Publ.	AU 2000033594
	Based on	WO 2000047996
CA 2359352	C Based on	WO 2000047996
AU 2004202799	A1 Div ex	AU 771458

PRIORITY APPLN. INFO: US 1999-119323P 19990209; US
 2000-500555 20000209; US
 2000-636387 20000809; US
 2001-925941 20010809; AU
 2004-202799 20040623

INT. PATENT CLASSIF.:

MAIN: B01J019-00; C12Q001-68; G01N033-50; G01N033-53
 SECONDARY: C07H021-04; G01N021-64; G01N021-77; G01N021-78;
 G01N033-48; G01N033-566; G01N037-00; G06F019-00;
 G06K009-00; G06T007-00

BASIC ABSTRACT:

WO 200047996 A UPAB: 20041104
 NOVELTY - **Array** composition (A) comprising a substrate (S) with

discrete sites on its surface, at least 2 subpopulations of microspheres (MS), each subpopulation including a bioactive agent (I), distributed over the surface of S, and at least 1 fiducial (F, i.e. a physical reference feature that allows precise comparison of sequential data images of the **array**), is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(a) system (B) comprising a computer-readable memory, for controlling a computer, consisting of modules for:

(i) recording a data image from a random **array** of discrete sites;

(ii) registering data images; and

(iii) comparing registered images;

(b) making (A) comprising forming a surface with individual sites on a substrate, distributing MS over the surface, and at least 1 F is incorporated into the surface

(c) computer-based comparison of separate data images of a random **array**;

(d) decoding a random **array** comprising treating an **array** (substrate plus MS) with many decoder binding ligands (DBLs) to create a data image, using F used to generate a registered data image, applying a second mixture of DBL and generating a second registered data image and comparing the images by computer to identify the locations of at least 2 (I); and

(e) determining presence of a target analyte (II) in a sample by comparing data images from an **array** as in (f), where the first and second images are registered before and after treatment of the **array** with a test sample.

USE - (A) is used to detect and quantify selected analytes (II), e.g. pollutants, therapeutic drugs, antigens, viruses, etc. particularly proteins and nucleic acids. Typical applications are in genetic diagnosis (e.g. of genes or mutations associated with cancer or Alzheimer's disease), screening blood for bacteria and viruses, monitoring of therapy, forensic DNA fingerprinting, and nucleic acid sequencing by hybridization. (A) are also useful in screening to identify agents that bind to, and preferably modify function of, a target molecule.

ADVANTAGE - The presence of F permits comparison of sequential images of (A), by preserving the relative positions of each site within the **array**. The synthesis and positioning of (I) can now be done separately, and the (I)-loaded MS can be distributed randomly, which is quicker and less expensive than in situ synthesis or spotting techniques. By using fiber optical techniques, **arrays** of very high density may be produced, e.g. about 25 million beads and fibers per 0.5 square cm. For quality control or calibration, the performance of every probe in every **array** can be tested by decoding with specific ligands.

Dwg.0/2

FILE SEGMENT:	CPI EPI
FIELD AVAILABILITY:	AB; DCN
MANUAL CODES:	CPI: B04-B04D5; B04-E05; B04-N04; B11-C07A; B11-C08E; B11-C08E5; B12-K04A; B12-K04A4; B12-K04E; B12-K04F; D05-H09; D05-H12D1; J04-B01
	EPI: S03-E14H

=> => fil capl
FILE 'CAPLUS' ENTERED AT 12:26:09 ON 23 FEB 2005
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
COPYRIGHT (C) 2005 AMERICAN CHEMICAL SOCIETY (ACS)

Copyright of the articles to which records in this database refer is held by the publishers listed in the PUBLISHER (PB) field (available for records published or updated in Chemical Abstracts after December 26, 1996), unless otherwise indicated in the original publications. The CA Lexicon is the copyrighted intellectual property of the American Chemical Society and is provided to assist you in searching databases on STN. Any dissemination, distribution, copying, or storing of this information, without the prior written consent of CAS, is strictly prohibited.

FILE COVERS 1907 - 23 Feb 2005 VOL 142 ISS 9
FILE LAST UPDATED: 22 Feb 2005 (20050222/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

'OBI' IS DEFAULT SEARCH FIELD FOR 'CAPLUS' FILE

=> d que l11; d que l15; d que l23

L2	1942	SEA	FILE=CAPLUS	ABB=ON	GENETIC/OBI (L) DATA#/OBI
L3	35148	SEA	FILE=CAPLUS	ABB=ON	ALLELE#/OBI
L4	42048	SEA	FILE=CAPLUS	ABB=ON	GENOTYP#/OBI
L5	58029	SEA	FILE=CAPLUS	ABB=ON	ARRAY#/OBI OR MICROARRAY#/OBI
L8	1	SEA	FILE=CAPLUS	ABB=ON	(SWEEP POINT#)/BI
L10	8	SEA	FILE=CAPLUS	ABB=ON	(REGISTRATION# (2A) TRANSFORM#)/BI
L11	0	SEA	FILE=CAPLUS	ABB=ON	(L8 OR L10) AND (L2 OR L3 OR L4 OR L5)

L2	1942	SEA	FILE=CAPLUS	ABB=ON	GENETIC/OBI (L) DATA#/OBI
L3	35148	SEA	FILE=CAPLUS	ABB=ON	ALLELE#/OBI
L4	42048	SEA	FILE=CAPLUS	ABB=ON	GENOTYP#/OBI
L5	58029	SEA	FILE=CAPLUS	ABB=ON	ARRAY#/OBI OR MICROARRAY#/OBI
L12	1218	SEA	FILE=CAPLUS	ABB=ON	TRIANGULAT#/BI
L13	237	SEA	FILE=CAPLUS	ABB=ON	DELAUNAY/BI
L15	0	SEA	FILE=CAPLUS	ABB=ON	L12 AND L13 AND (L2 OR L3 OR L4 OR L5)

L7	3991	SEA	FILE=CAPLUS	ABB=ON	(COORDINATE SYSTEM#)/BI
L9	1321	SEA	FILE=CAPLUS	ABB=ON	(CONTROL POINT#)/BI
L23	0	SEA	FILE=CAPLUS	ABB=ON	L7 AND L9

=> d que l17; d que l19; d que l24; d que l33

L2	1942	SEA	FILE=CAPLUS	ABB=ON	GENETIC/OBI (L) DATA#/OBI
L6	5097	SEA	FILE=CAPLUS	ABB=ON	NORMALIZ#/OBI
L17	3	SEA	FILE=CAPLUS	ABB=ON	L2 AND L6

L3 35148 SEA FILE=CAPLUS ABB=ON ALLELE#/OBI
 L4 42048 SEA FILE=CAPLUS ABB=ON GENOTYP#/OBI
 L6 5097 SEA FILE=CAPLUS ABB=ON NORMALIZ#/OBI
 L18 16 SEA FILE=CAPLUS ABB=ON (L3 OR L4) AND L6
 L19 4 SEA FILE=CAPLUS ABB=ON L18 AND DNA/TI

L2 1942 SEA FILE=CAPLUS ABB=ON GENETIC/OBI (L) DATA#/OBI
 L3 35148 SEA FILE=CAPLUS ABB=ON ALLELE#/OBI
 L4 42048 SEA FILE=CAPLUS ABB=ON GENOTYP#/OBI
 L7 3991 SEA FILE=CAPLUS ABB=ON (COORDINATE SYSTEM#)/BI
 L24 1 SEA FILE=CAPLUS ABB=ON L7 AND (L2 OR L3 OR L4)

L2 1942 SEA FILE=CAPLUS ABB=ON GENETIC/OBI (L) DATA#/OBI
 L3 35148 SEA FILE=CAPLUS ABB=ON ALLELE#/OBI
 L4 42048 SEA FILE=CAPLUS ABB=ON GENOTYP#/OBI
 L5 58029 SEA FILE=CAPLUS ABB=ON ARRAY#/OBI OR MICROARRAY#/OBI
 L6 5097 SEA FILE=CAPLUS ABB=ON NORMALIZ#/OBI
 L7 3991 SEA FILE=CAPLUS ABB=ON (COORDINATE SYSTEM#)/BI
 L8 1 SEA FILE=CAPLUS ABB=ON (SWEEP POINT#)/BI
 L9 1321 SEA FILE=CAPLUS ABB=ON (CONTROL POINT#)/BI
 L10 8 SEA FILE=CAPLUS ABB=ON (REGISTRATION# (2A) TRANSFORM#)/BI
 L12 1218 SEA FILE=CAPLUS ABB=ON TRIANGULAT#/BI
 L13 237 SEA FILE=CAPLUS ABB=ON DELAUNAY/BI
 L14 55 SEA FILE=CAPLUS ABB=ON L12 AND L13
 L33 1 SEA FILE=CAPLUS ABB=ON L14 AND (L2 OR L3 OR L4 OR L5 OR L6 OR L7 OR L8 OR L9 OR L10)

=> s l17 or l19 or l24 or l33

L92 9 L17 OR L19 OR L24 OR L33

=> fil wpids

FILE 'WPIDS' ENTERED AT 12:26:12 ON 23 FEB 2005
 COPYRIGHT (C) 2005 THE THOMSON CORPORATION

FILE LAST UPDATED: 18 FEB 2005 <20050218/UP>
 MOST RECENT DERWENT UPDATE: 200512 <200512/DW>
 DERWENT WORLD PATENTS INDEX SUBSCRIBER FILE, COVERS 1963 TO DATE

>>> FOR A COPY OF THE DERWENT WORLD PATENTS INDEX STN USER GUIDE,
 PLEASE VISIT:
http://www.stn-international.de/training_center/patents/stn_guide.pdf <<<

>>> FOR DETAILS OF THE PATENTS COVERED IN CURRENT UPDATES, SEE
<http://thomsonderwent.com/coverage/latestupdates/> <<<

>>> FOR INFORMATION ON ALL DERWENT WORLD PATENTS INDEX USER
 GUIDES, PLEASE VISIT:
<http://thomsonderwent.com/support/userguides/> <<<

>>> NEW! FAST-ALERTING ACCESS TO NEWLY-PUBLISHED PATENT
 DOCUMENTATION NOW AVAILABLE IN DERWENT WORLD PATENTS INDEX
 FIRST VIEW - FILE WPIFV.
 FOR FURTHER DETAILS: <http://www.thomsonderwent.com/dwpifv> <<<

>>> NEW DISPLAY FORMAT HITSTR ADDED ALLOWING DISPLAY OF
HIT STRUCTURES WITHIN THE BIBLIOGRAPHIC DOCUMENT <<<

>>> SMILES and ISOSMILES strings are no longer available as
Derwent Chemistry Resource display fields <<<

>>> THE CPI AND EPI MANUAL CODES HAVE BEEN REVISED FROM UPDATE 200501.
PLEASE CHECK:

<http://thomsonderwent.com/support/dwpioref/reftools/classification/code-revision/>
FOR DETAILS. <<<

=> d que 152; d que 157

```
L35      3564 SEA FILE=WPIDS ABB=ON ALLELE#
L36      2764 SEA FILE=WPIDS ABB=ON GENOTYP?
L38      3468 SEA FILE=WPIDS ABB=ON MICROARRAY#
L41      15 SEA FILE=WPIDS ABB=ON SWEEP POINT#
L43      581 SEA FILE=WPIDS ABB=ON (REGISTRATION OR CONFORMATION? OR
      PROJECT?) (3A) TRANSFORM?
L44      31 SEA FILE=WPIDS ABB=ON DELAUNAY
L46      49 SEA FILE=WPIDS ABB=ON GENETIC DATA#
L52      0 SEA FILE=WPIDS ABB=ON (L35 OR L36 OR L38 OR L46) AND (L41 OR
      L43 OR L44)
```

```
L39      15854 SEA FILE=WPIDS ABB=ON NORMALI?
L46      49 SEA FILE=WPIDS ABB=ON GENETIC DATA#
L57      0 SEA FILE=WPIDS ABB=ON L46 AND L39
```

=> d que 154; d que 158; d que 159

```
L44      31 SEA FILE=WPIDS ABB=ON DELAUNAY
L45      1584 SEA FILE=WPIDS ABB=ON TRIANGULAT?
L53      13 SEA FILE=WPIDS ABB=ON L44 AND L45
L54      2 SEA FILE=WPIDS ABB=ON L53 AND MOLECUL?/TI
```

```
L35      3564 SEA FILE=WPIDS ABB=ON ALLELE#
L36      2764 SEA FILE=WPIDS ABB=ON GENOTYP?
L37      156518 SEA FILE=WPIDS ABB=ON ARRAY#
L38      3468 SEA FILE=WPIDS ABB=ON MICROARRAY#
L40      7980 SEA FILE=WPIDS ABB=ON (COORDINATE OR CO ORDINATE) (2A) SYSTEM#
L41      15 SEA FILE=WPIDS ABB=ON SWEEP POINT#
L43      581 SEA FILE=WPIDS ABB=ON (REGISTRATION OR CONFORMATION? OR
      PROJECT?) (3A) TRANSFORM?
L44      31 SEA FILE=WPIDS ABB=ON DELAUNAY
L46      49 SEA FILE=WPIDS ABB=ON GENETIC DATA#
L49      29 SEA FILE=WPIDS ABB=ON ((L35 OR L36 OR L37 OR L38) OR L46) AND
      (L41 OR L43 OR L44)
L56      18 SEA FILE=WPIDS ABB=ON L40 AND L43
L58      1 SEA FILE=WPIDS ABB=ON L56 AND ((L35 OR L36 OR L37 OR L38) OR
      L49)
```

```
L42      3946 SEA FILE=WPIDS ABB=ON CONTROL POINT#
L43      581 SEA FILE=WPIDS ABB=ON (REGISTRATION OR CONFORMATION? OR
      PROJECT?) (3A) TRANSFORM?
L59      2 SEA FILE=WPIDS ABB=ON L42 AND L43
```

=> s 154 or 158 or 159

L93 5 L54 OR L58 OR L59

=> fil JICST-EPLUS, PASCAL, BIOTECHNO, ESBIODBASE, BIOSIS, DISSABS, JAPIO, INSPEC, COMPENDEX, COMPUSCIENCE, COMPUAB, SCISEARCH

FILE 'JICST-EPLUS' ENTERED AT 12:26:16 ON 23 FEB 2005
COPYRIGHT (C) 2005 Japan Science and Technology Agency (JST)

FILE 'PASCAL' ENTERED AT 12:26:16 ON 23 FEB 2005
Any reproduction or dissemination in part or in full,
by means of any process and on any support whatsoever
is prohibited without the prior written agreement of INIST-CNRS.
COPYRIGHT (C) 2005 INIST-CNRS. All rights reserved.

FILE 'BIOTECHNO' ENTERED AT 12:26:16 ON 23 FEB 2005
COPYRIGHT (C) 2005 Elsevier Science B.V., Amsterdam. All rights reserved.

FILE 'ESBIODBASE' ENTERED AT 12:26:16 ON 23 FEB 2005
COPYRIGHT (C) 2005 Elsevier Science B.V., Amsterdam. All rights reserved.

FILE 'BIOSIS' ENTERED AT 12:26:16 ON 23 FEB 2005
Copyright (c) 2005 The Thomson Corporation.

FILE 'DISSABS' ENTERED AT 12:26:16 ON 23 FEB 2005
COPYRIGHT (C) 2005 ProQuest Information and Learning Company; All Rights Reserved.

FILE 'JAPIO' ENTERED AT 12:26:16 ON 23 FEB 2005
COPYRIGHT (C) 2005 Japanese Patent Office (JPO)- JAPIO

FILE 'INSPEC' ENTERED AT 12:26:16 ON 23 FEB 2005
Compiled and produced by the IEE in association with FIZ KARLSRUHE
COPYRIGHT 2005 (c) INSTITUTION OF ELECTRICAL ENGINEERS (IEE)

FILE 'COMPENDEX' ENTERED AT 12:26:16 ON 23 FEB 2005
Compendex Compilation and Indexing (C) 2005
Elsevier Engineering Information Inc (EEI). All rights reserved.
Compendex (R) is a registered Trademark of Elsevier Engineering Information Inc.

FILE 'COMPUSCIENCE' ENTERED AT 12:26:16 ON 23 FEB 2005
COPYRIGHT (c) 2005 FACHINFORMATIONSZENTRUM KARLSRUHE (FIZ KARLSRUHE)

FILE 'COMPUAB' ENTERED AT 12:26:16 ON 23 FEB 2005
COPYRIGHT (C) 2005 Cambridge Scientific Abstracts (CSA)

FILE 'SCISEARCH' ENTERED AT 12:26:16 ON 23 FEB 2005
Copyright (c) 2005 The Thomson Corporation.

=> d que 178; d que 177; d que 182

L62 315958 SEA ALLELE#
L63 367676 SEA GENOTYP?
L64 1845597 SEA GENETIC
L65 691272 SEA ARRAY#
L66 55463 SEA MICROARRAY#
L67 302708 SEA NORMALIZ? OR NORMALIS?
L68 41265 SEA (COORDINATE OR CO ORDINATE) (W) SYSTEM#
L69 19 SEA SWEEP POINT#
L70 16525 SEA CONTROL POINT#

L71 5953 SEA DELAUNAY
 L72 30643 SEA TRIANGULAT?
 L73 6608 SEA (REGIST? OR CONFORMATION? OR PROJECT?) (3A) TRANSFORM?
 L78 0 SEA L69 AND ((L62 OR L63 OR L64 OR L65 OR L66 OR L67 OR L68)
 OR (L70 OR L71 OR L72 OR L73))

L62 315958 SEA ALLELE#
 L63 367676 SEA GENOTYP?
 L64 1845597 SEA GENETIC
 L67 302708 SEA NORMALIZ? OR NORMALIS?
 L68 41265 SEA (COORDINATE OR CO ORDINATE) (W) SYSTEM#
 L76 7433 SEA L67 AND (L62 OR L63 OR L64)
 L77 0 SEA L76 AND L68

L62 315958 SEA ALLELE#
 L63 367676 SEA GENOTYP?
 L64 1845597 SEA GENETIC
 L67 302708 SEA NORMALIZ? OR NORMALIS?
 L68 41265 SEA (COORDINATE OR CO ORDINATE) (W) SYSTEM#
 L70 16525 SEA CONTROL POINT#
 L71 5953 SEA DELAUNAY
 L72 30643 SEA TRIANGULAT?
 L73 6608 SEA (REGIST? OR CONFORMATION? OR PROJECT?) (3A) TRANSFORM?
 L79 30 SEA L71 AND L72 AND (L62 OR L63 OR L64)
 L82 0 SEA L79 AND (L68 OR L70 OR L73 OR L67)

=> d que 183; d que 185; d que 190

L62 315958 SEA ALLELE#
 L63 367676 SEA GENOTYP?
 L64 1845597 SEA GENETIC
 L65 691272 SEA ARRAY#
 L66 55463 SEA MICROARRAY#
 L71 5953 SEA DELAUNAY
 L72 30643 SEA TRIANGULAT?
 L79 30 SEA L71 AND L72 AND (L62 OR L63 OR L64)
 L83 2 SEA L79 AND (L65 OR L66)

L62 315958 SEA ALLELE#
 L63 367676 SEA GENOTYP?
 L64 1845597 SEA GENETIC
 L71 5953 SEA DELAUNAY
 L72 30643 SEA TRIANGULAT?
 L85 19 SEA L71(L) L72(L) (L62 OR L63 OR L64)

L62 315958 SEA ALLELE#
 L63 367676 SEA GENOTYP?
 L64 1845597 SEA GENETIC
 L65 691272 SEA ARRAY#
 L66 55463 SEA MICROARRAY#
 L67 302708 SEA NORMALIZ? OR NORMALIS?
 L68 41265 SEA (COORDINATE OR CO ORDINATE) (W) SYSTEM#
 L70 16525 SEA CONTROL POINT#

L71 5953 SEA DELAUNAY
 L72 30643 SEA TRIANGULAT?
 L73 6608 SEA (REGIST? OR CONFORMATION? OR PROJECT?) (3A) TRANSFORM?
 L89 160 SEA (L62 OR L63 OR L64) AND L68
 L90 7 SEA L89 AND ((L65 OR L66 OR L67) OR (L70 OR L71 OR L72 OR L73))

=> s 183 or 185 or 190

L94 26 L83 OR L85 OR L90

=> => dup rem 192,194,193

FILE 'CAPLUS' ENTERED AT 12:26:54 ON 23 FEB 2005
 USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
 PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
 COPYRIGHT (C) 2005 AMERICAN CHEMICAL SOCIETY (ACS)

FILE 'JICST-EPLUS' ENTERED AT 12:26:54 ON 23 FEB 2005
 COPYRIGHT (C) 2005 Japan Science and Technology Agency (JST)

FILE 'PASCAL' ENTERED AT 12:26:54 ON 23 FEB 2005
 Any reproduction or dissemination in part or in full,
 by means of any process and on any support whatsoever
 is prohibited without the prior written agreement of INIST-CNRS.
 COPYRIGHT (C) 2005 INIST-CNRS. All rights reserved.

FILE 'ESBIOBASE' ENTERED AT 12:26:54 ON 23 FEB 2005
 COPYRIGHT (C) 2005 Elsevier Science B.V., Amsterdam. All rights reserved.

FILE 'INSPEC' ENTERED AT 12:26:54 ON 23 FEB 2005
 Compiled and produced by the IEE in association with FIZ KARLSRUHE
 COPYRIGHT 2005 (c) INSTITUTION OF ELECTRICAL ENGINEERS (IEE)

FILE 'COMPENDEX' ENTERED AT 12:26:54 ON 23 FEB 2005
 Compendex Compilation and Indexing (C) 2005
 Elsevier Engineering Information Inc (EEI). All rights reserved.
 Compendex (R) is a registered Trademark of Elsevier Engineering Information Inc.

FILE 'COMPUSCIENCE' ENTERED AT 12:26:54 ON 23 FEB 2005
 COPYRIGHT (c) 2005 FACHINFORMATIONSZENTRUM KARLSRUHE (FIZ KARLSRUHE)

FILE 'SCISEARCH' ENTERED AT 12:26:54 ON 23 FEB 2005
 Copyright (c) 2005 The Thomson Corporation.

FILE 'WPIDS' ENTERED AT 12:26:54 ON 23 FEB 2005
 COPYRIGHT (C) 2005 THE THOMSON CORPORATION
 PROCESSING COMPLETED FOR L92
 PROCESSING COMPLETED FOR L94
 PROCESSING COMPLETED FOR L93

L95 31 DUP REM L92 L94 L93 (9 DUPLICATES REMOVED)
 ANSWERS '1-9' FROM FILE CAPLUS
 ANSWERS '10-12' FROM FILE JICST-EPLUS
 ANSWERS '13-15' FROM FILE PASCAL
 ANSWER '16' FROM FILE ESBIOBASE
 ANSWERS '17-25' FROM FILE INSPEC
 ANSWER '26' FROM FILE COMPUSCIENCE
 ANSWERS '27-31' FROM FILE WPIDS

=> d ibib ed abs hitind 1-9; d iall 10-31; fil hom

L95 ANSWER 1 OF 31 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2005:14597 CAPLUS
 DOCUMENT NUMBER: 142:108376
 TITLE: Mutation/polymorphism analysis by DNA
 microarray with matching and mismatching probes and
 signal correction
 INVENTOR(S): Nagaoka, Tomonori
 PATENT ASSIGNEE(S): Olympus Corporation, Japan
 SOURCE: PCT Int. Appl., 51 pp.
 CODEN: PIXXD2
 DOCUMENT TYPE: Patent
 LANGUAGE: Japanese
 FAMILY ACC. NUM. COUNT: 1
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2005001125	A1	20050106	WO 2004-JP9275	20040624
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW			
RW:	BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			

PRIORITY APPLN. INFO.: JP 2003-184474 A 20030627

ED Entered STN: 07 Jan 2005

AB Provide a means of, in analyzing mutations or polymorphisms with the use of a DNA microarray, identifying whether a signal from each of spots on the DNA microarray perfectly or imperfectly matches between a probe and a target nucleic acid, even in the case of using a sample nucleic acid mol. having a hetero (heterozygous/heterogeneous) sequence. A method is characterized by using a sample exclusively having candidates for a perfectly matching probe and a perfectly matching nucleic acid, subtracting the signal data thus obtained from untreated data to thereby correct signal values caused by nonspecific hybridization, and, in the case where the corrected signal value amts. to a certain level or higher, identifying the signal as originating in perfect matching. A rapid, precise, and accurate microarray-based method has been developed that uses a signal data normalization for detection of mutations. Authors used the DNA microarray to detect mutations in codon 12 of K-ras. Fluorescein isothiocyanate-labeled PCR products were analyzed with the microarray. Authors could correctly identify wild-type, heterozygous, and homozygous mutant genotypes with the DNA microarray in <3.5 h. This is a novel DNA microarray system and can be used to analyze K-ras mutations quickly and accurately.

IC ICM C12Q001-68

ICS C12N015-09; C12M001-00; G01N033-53; G01N033-566; G01N037-00

CC 3-1 (Biochemical Genetics)

Section cross-reference(s): 9

ST mutation polymorphism DNA microarray analysis matching mismatching probe; signal **normalization** data correction DNA microarray mutation polymorphism

IT DNA microarray technology

Genetic polymorphism

Genotyping (method)

Mutation

(mutation/polymorphism anal. by DNA microarray with matching and mismatching probes and signal correction)

IT Data processing

(**normalization**; mutation/polymorphism anal. by DNA microarray
with matching and mismatching probes and signal correction)

REFERENCE COUNT: 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS
RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L95 ANSWER 2 OF 31 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2004:27135 CAPLUS

DOCUMENT NUMBER: 140:289452

TITLE: Process design optimisation using embedded hybrid
visualization and **data** analysis techniques
within a **genetic** algorithm optimisation
framework

AUTHOR(S): Wang, K.; Salhi, A.; Fraga, E. S.

CORPORATE SOURCE: Centre for Process Systems Engineering, Department of
Chemical Engineering, University College London (UCL),
London, WC1E 7JE, UK

SOURCE: Chemical Engineering and Processing (2004), 43(5),
657-669

CODEN: CENPEU; ISSN: 0255-2701

PUBLISHER: Elsevier Science B.V.

DOCUMENT TYPE: Journal

LANGUAGE: English

ED Entered STN: 13 Jan 2004

AB Process optimization is a difficult task due to the non-linear, non-convex
and often discontinuous nature of the math. models used. Although
significant advances in deterministic methods were made, stochastic
procedures, specifically genetic algorithms, provide an attractive
technol. for solving these optimization problems. However, genetic
algorithms are not naturally suited to highly constrained problems. We
propose a targeted genetic algorithm for process optimization which is
suitable for highly constrained problems. The genetic operators,
crossover and mutation, are defined based on information gained about the
feasible region and the behavior of the objective function through the use
of a data anal. procedure. The data anal. is based on a visual
representation, the parallel **coordinate system**. A
pattern matching algorithm, the Scan Circle Algorithm [K. Wang, A. Salhi,
E.S. Fraga, Cluster identification using a parallel **coordinate**
system for knowledge discovery and nonlinear optimization, in: J.
Grievink, J. van Schijndel (Eds.), Proceedings of the 12th European
Symposium on Computer-Aided Process Engineering, Computer-Aided Chemical
Engineering, volume 10, Elsevier, Amsterdam, 2002, pp. 1003-1008], is
extended through the use of Learning Vector Quantization [T. Kohonen,
Self-Organizing Maps, Springer-Verlag, Heidelberg, 1995] to identify,
automatically, key features of the objective function and the search
space. These features are used to target the genetic operators. Results
from the application of the new targeted genetic algorithm to an oil
stabilization problem are presented, demonstrating the effective,
efficient and robust nature of the implementation. The use of
visualization as the core of the data anal. step also provides a useful
tool for explaining the results obtained by the optimization procedure.

CC 48-10 (Unit Operations and Processes)

ST design optimization visualization **data genetic**
algorithm

IT Algorithm

(**genetic**; process design optimization using embedded hybrid
visualization and **data** anal. techniques within
genetic algorithm optimization framework)

IT Optimization

(nonlinear; process design optimization using embedded hybrid
visualization and **data** anal. techniques within
genetic algorithm optimization framework)

IT Chemical engineering design

(process design optimization using embedded hybrid visualization and
data anal. techniques within **genetic** algorithm
optimization framework)

REFERENCE COUNT: 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS
RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L95 ANSWER 3 OF 31 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2004:407896 CAPLUS

DOCUMENT NUMBER: 141:119618

TITLE: Fast automatic registration of images using the phase
of a complex wavelet transform: application to
proteome gels

AUTHOR(S): Woodward, Andrew M.; Rowland, Jem J.; Kell, Douglas B.

CORPORATE SOURCE: Institute of Biological Sciences, University of Wales,
Aberystwyth, SY23 3DD, UK

SOURCE: Analyst (Cambridge, United Kingdom) (2004), 129(6),
542-552

CODEN: ANALAO; ISSN: 0003-2654

PUBLISHER: Royal Society of Chemistry

DOCUMENT TYPE: Journal

LANGUAGE: English

ED Entered STN: 20 May 2004

AB Image registration describes the process of manipulating a distorted
version of an image such that its pixels overlay the equivalent pixels in a
clean, master or reference image. The need for it has assumed particular
prominence in the anal. of images of electrophoretic gels used in the
anal. of protein expression levels in living cells, but also has
fundamental applications in most other areas of image anal. Much of the
positional information of a data feature is carried in the phase of a
complex transform, so a complex transform allows explicit specification of
the phase, and hence of the position of features in the image.
Registration of a test gel to a reference gel is achieved by using a
multiresoln. movement map derived from the phase of a complex wavelet
transform (the Q-shift wavelet transform) to dictate the warping directly
via movement of the nodes of a **Delaunay-triangulated**
mesh of points. This warping map is then applied to the original
untransformed image such that the absolute magnitude of the spots remains
unchanged. The technique is general to any type of image. Results are
presented for a simple computer simulated gel, a simple real gel
registration between similar "clean" gels with local warping vectors
distributed about one main direction, a hard problem between a reference gel
and a "dirty" test gel with multi-directional warping vectors and many
artifacts, and some typical gels of present interest in post-genomic biol.
The method compares favorably with others, since it is computationally
rapid, effective and entirely automatic.

CC 9-7 (Biochemical Methods)

Section cross-reference(s): 6, 10

ST protein QSWT automatic **registration** wavelet **transform**

proteome gel electrophoresis

IT Algorithm

(DTWT (dual tree wavelet complex **transform**); fast automatic
registration of images using the phase of complex wavelet
transform for proteome 2-D gels)

IT Algorithm

(QSWT (Q-shift **transform**); fast automatic
registration of images using the phase of complex wavelet
transform for proteome 2-D gels)

REFERENCE COUNT: 95 THERE ARE 95 CITED REFERENCES AVAILABLE FOR THIS
RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L95 ANSWER 4 OF 31 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2003:686485 CAPLUS
DOCUMENT NUMBER: 139:318111
TITLE: Quantification of single nucleotide polymorphisms by automated DNA sequencing
AUTHOR(S): Qiu, Ping; Soder, George J.; Sanfiorenzo, Vincent J.; Wang, Luquan; Greene, Jonathan R.; Fritz, Mary Ann; Cai, Xiao-Yan
CORPORATE SOURCE: Bioinformatics Group and Discovery Technology Department, Schering-Plough Research Institute, Kenilworth, NJ, 07033, USA
SOURCE: Biochemical and Biophysical Research Communications (2003), 309(2), 331-338
CODEN: BBRCA9; ISSN: 0006-291X
PUBLISHER: Elsevier Science
DOCUMENT TYPE: Journal
LANGUAGE: English
ED Entered STN: 03 Sep 2003
AB Single nucleotide polymorphisms (SNPs) are linked to phenotypes associated with diseases and drug responses. Many techniques are now available to identify and quantify such SNPs in DNA or RNA pools, although the information on the latter is limited. The majority of these methodologies require prior knowledge of target sequences, normally obtained through DNA sequencing. Direct quantitation of SNPs from DNA sequencing raw data will save time and money for large amount sample anal. A high throughput DNA sequencing assay, in combination with a SNP quant. algorithm, was developed for the quantitation of a SNP present in HCV RNA sequences. For a side-by-side comparison, a Pyrosequencing assay was also developed. Quantitation performance was evaluated for both methods. The direct DNA sequencing quantitation method was shown to be more linear, accurate, sensitive, and reproducible than the Pyrosequencing method for the quantitation of the SNP present in HCV RNA mols.
CC 3-1 (Biochemical Genetics)
Section cross-reference(s): 10
IT **Genotypes**
(heterozygosity, quantitation of; quantification of single nucleotide polymorphisms by automated DNA sequencing)
IT Algorithm
(**normalize** peak height, report background level, quantify heterozygous bases; quantification of single nucleotide polymorphisms by automated DNA sequencing)
REFERENCE COUNT: 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L95 ANSWER 5 OF 31 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2002:250454 CAPLUS
DOCUMENT NUMBER: 137:120237
TITLE: **Normalization** of cDNA microarray data using exogenous nucleic acid control in gene differential expression determination
AUTHOR(S): Zhang, Liang; Zhang, Jian; Zhou, Yu-xiang; Cheng, Jing
CORPORATE SOURCE: Department of Biological Science and Technology, Tsinghua University, Beijing, 100084, Peop. Rep. China
SOURCE: Zhongguo Shengwu Huaxue Yu Fenzi Shengwu Xuebao (2002), 18(1), 115-119
CODEN: ZSHXF2; ISSN: 1007-7626
PUBLISHER: Zhongguo Shengwu Huaxue Yu Fenzi Shengwu Xuebao
DOCUMENT TYPE: Journal
LANGUAGE: Chinese
ED Entered STN: 04 Apr 2002
AB In DNA microarray technol., it is necessary to determine the detection sensitivity level and normalize the difference in Dye incorporation and

quantum yield. In the past, the housekeeping genes were frequently used to normalize the microarray data. However, more recent reports indicate that the expression levels of housekeeping genes can vary. Three exogenous polyadenylated RNA were produced through in vitro transcription and used as internal control RNA, standing for high, medium and low abundance resp. The result showed that the fluorescent signal intensity of hybridization was pos. correlative with the gene transcript abundance and gene differential expression was identified in both DNA microarray and Northern blot methods.

CC 3-1 (Biochemical Genetics)

IT Gene

RL: BSU (Biological study, unclassified); BIOL (Biological study)
(expression; **normalization** of cDNA microarray data using
exogenous nucleic acid control in gene differential expression determination)

IT DNA microarray technology

Transcription, **genetic**

(**normalization** of cDNA microarray data using
exogenous nucleic acid control in gene differential expression determination)

IT RNA

RL: BSU (Biological study, unclassified); BIOL (Biological study)
(poly(A)-containing; **normalization** of cDNA microarray data using
exogenous nucleic acid control in gene differential expression determination)

L95 ANSWER 6 OF 31 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2002:565465 CAPLUS

DOCUMENT NUMBER: 138:52111

TITLE: Knowledge-based image processing for on-off type
DNA microarray

AUTHOR(S): Kim, Jong Dae; Kim, Seo Kyu; Cho, Jeong Sik; Kim,
Jongwon

CORPORATE SOURCE: Div. of Inform. and Comm. Eng., Hallym University,
Chunchon, S. Korea

SOURCE: Proceedings of SPIE-The International Society for
Optical Engineering (2002), 4623(Functional Monitoring
and Drug-Tissue Interaction), 38-46
CODEN: PSISDG; ISSN: 0277-786X

PUBLISHER: SPIE-The International Society for Optical Engineering

DOCUMENT TYPE: Journal

LANGUAGE: English

ED Entered STN: 31 Jul 2002

AB This paper addresses the image processing technique for discriminating whether the probes are hybridized with target DNA in the Human Papilloma Virus (HPV) DNA Chip designed for genotyping HPV. In addition to the probes, the HPV DNA chip has markers that always react with the sample DNA. The positions of probe-dots in the final scanned image are fixed relative to the marker-dot locations with a small variation according to the accuracy of the dotter and the scanner. The probes are duplicated 4 times for the diagnostic stability. The prior knowledges such as the maker relative distance and the duplication information of probes is integrated into the template matching technique with the normalized correlation measure. Results show that the employment of both of the prior knowledges is to simply average the template matching measures over the positions of the markers and probes. The eventual proposed scheme yields stable marker locating and probe classification.

CC 9-1 (Biochemical Methods)

Section cross-reference(s): 3, 20

IT Human papillomavirus

(HPV, DNA Chip **genotyping**; knowledge-based image processing
for on-off type HPV DNA microarray)

IT Statistical analysis

(**normalized** correlation, for marker locating and probe
classification; knowledge-based image processing for on-off type HPV)

DNA microarray)

REFERENCE COUNT: 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L95 ANSWER 7 OF 31 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2002:597001 CAPLUS

DOCUMENT NUMBER: 138:101428

TITLE: Accurate **normalization** of real-time quantitative RT-PCR data by geometric averaging of multiple internal control genes

AUTHOR(S): Vandesompele, Jo; De Preter, Katleen; Pattyn, Filip; Poppe, Bruce; Van Roy, Nadine; De Paepe, Anne; Speleman, Frank

CORPORATE SOURCE: Center for Medical Genetics, Ghent University Hospital 1K5, Ghent, B-9000, Belg.

SOURCE: GenomeBiology [online computer file] (2002), 3(7), No pp. given

CODEN: GNBLEW; ISSN: 1465-6914

URL: <http://genomebiology.com/2002/3/7/research/0034.1>

PUBLISHER: BioMed Central Ltd.

DOCUMENT TYPE: Journal; (online computer file)

LANGUAGE: English

ED Entered STN: 12 Aug 2002

AB Background: Gene-expression anal. is increasingly important in biol. research, with real-time reverse transcription PCR (RT-PCR) becoming the method of choice for high-throughput and accurate expression profiling of selected genes. Given the increased sensitivity, reproducibility and large dynamic range of this methodol., the requirements for a proper internal control gene for normalization have become increasingly stringent. Although housekeeping gene expression has been reported to vary considerably, no systematic survey has properly determined the errors related to the common practice of using only one control gene, nor presented an adequate way of working around this problem. Results: We outline a robust and innovative strategy to identify the most stably expressed control genes in a given set of tissues, and to determine the min. number of genes required to calculate a reliable normalization factor. We have evaluated ten housekeeping genes from different abundance and functional classes in various human tissues, and demonstrated that the conventional use of a single gene for normalization leads to relatively large errors in a significant proportion of samples tested. The geometric mean of multiple carefully selected housekeeping genes was validated as an accurate normalization factor by analyzing publicly available microarray data. Conclusions: The normalization strategy presented here is a prerequisite for accurate RT-PCR expression profiling, which, among other things, opens up the possibility of studying the biol. relevance of small expression differences.

CC 3-1 (Biochemical Genetics)

Section cross-reference(s): 6, 7, 13

IT Proteins

RL: BSU (Biological study, unclassified); BIOL (Biological study)

(14-3-3, zeta subunit, use as internal housekeeping gene control of gene YWHAZ for; accurate **normalization** of real-time quant.

RT-PCR data by geometric averaging of multiple internal housekeeping gene controls)

IT Ribosomal proteins

RL: BSU (Biological study, unclassified); BIOL (Biological study)

(L13a, use as internal housekeeping gene control of gene RPL13A for; accurate **normalization** of real-time quant. RT-PCR data by

geometric averaging of multiple internal housekeeping gene controls)

IT PCR (polymerase chain reaction)

(RT-PCR (reverse transcription-PCR), real-time quant.; accurate **normalization** of real-time quant. RT-PCR data by geometric

- averaging of multiple internal control genes)
- IT Human
(RT-PCR for human gene targets; accurate **normalization** of real-time quant. RT-PCR data by geometric averaging of multiple internal housekeeping gene controls)
- IT Transcription factors
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(TBP (TATA box-binding protein), use as internal housekeeping gene control of gene TBP for; accurate **normalization** of real-time quant. RT-PCR data by geometric averaging of multiple internal housekeeping gene controls)
- IT Primers (nucleic acid)
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(for internal housekeeping gene controls in RT-PCR; accurate **normalization** of real-time quant. RT-PCR data by geometric averaging of multiple internal housekeeping gene controls)
- IT **Genetic methods**
(gene expression profiling by RT-PCR; accurate **normalization** of real-time quant. RT-PCR data by geometric averaging of multiple internal control genes)
- IT Gene, animal
RL: ARU (Analytical role, unclassified); ANST (Analytical study)
(housekeeping genes; accurate **normalization** of real-time quant. RT-PCR data by geometric averaging of multiple internal housekeeping gene controls)
- IT Gene expression profiles, animal
(of housekeeping genes; accurate **normalization** of real-time quant. RT-PCR data by geometric averaging of multiple internal control genes)
- IT Actins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(β -, use as internal housekeeping gene control of gene ACTB for; accurate **normalization** of real-time quant. RT-PCR data by geometric averaging of multiple internal housekeeping gene controls)
- IT Microglobulins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(β 2-, use as internal housekeeping gene control of gene B2M for; accurate **normalization** of real-time quant. RT-PCR data by geometric averaging of multiple internal housekeeping gene controls)
- IT 9016-12-0, Hypoxanthine phosphoribosyl transferase
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(I, use as internal housekeeping gene control of gene HPRT1 for; accurate **normalization** of real-time quant. RT-PCR data by geometric averaging of multiple internal housekeeping gene controls)
- IT 485877-14-3 485877-15-4 485877-16-5 485877-17-6 485877-18-7
485877-19-8 485877-20-1 485877-21-2 485877-22-3 485877-23-4
485877-24-5 485877-25-6 485877-26-7 485877-27-8 485877-28-9
485877-29-0 485877-30-3 485877-31-4
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(PCR primer; accurate **normalization** of real-time quant. RT-PCR data by geometric averaging of multiple internal housekeeping gene controls)
- IT 9002-02-2, Succinate dehydrogenase
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(subunit A, use as internal housekeeping gene control of gene SDHA for; accurate **normalization** of real-time quant. RT-PCR data by geometric averaging of multiple internal housekeeping gene controls)
- IT 9001-50-7, Glyceraldehyde-3-phosphate dehydrogenase
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(use as internal housekeeping gene control of gene GAPD for; accurate

normalization of real-time quant. RT-PCR data by geometric averaging of multiple internal housekeeping gene controls)

IT 9074-91-3, Hydroxymethyl-bilane synthase
 RL: BSU (Biological study, unclassified); BIOL (Biological study)
 (use as internal housekeeping gene control of gene HMBS for; accurate **normalization** of real-time quant. RT-PCR data by geometric averaging of multiple internal housekeeping gene controls)

IT 151821-62-4, Ubiquitin C
 RL: BSU (Biological study, unclassified); BIOL (Biological study)
 (use as internal housekeeping gene control of gene UBC for; accurate **normalization** of real-time quant. RT-PCR data by geometric averaging of multiple internal housekeeping gene controls)

REFERENCE COUNT: 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L95 ANSWER 8 OF 31 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2001:101364 CAPLUS
 DOCUMENT NUMBER: 134:159830
 TITLE: Methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing
 INVENTOR(S): Hadd, Andy; Jovanovich, Stevan
 PATENT ASSIGNEE(S): Molecular Dynamics, Inc., USA
 SOURCE: PCT Int. Appl., 131 pp.
 CODEN: PIXXD2
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 5
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001009389	A2	20010208	WO 2000-US21182	20000802
WO 2001009389	A3	20010816		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
US 6423536	B1	20020723	US 2000-577199	20000523
CA 2380794	AA	20010208	CA 2000-2380794	20000802
EP 1203099	A2	20020508	EP 2000-952450	20000802
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL				
JP 2003505110	T2	20030212	JP 2001-513644	20000802
PRIORITY APPLN. INFO.:			US 1999-146732P	P 19990802
			US 2000-577199	A 20000523
			WO 2000-US21182	W 20000802

ED Entered STN: 09 Feb 2001

AB Methods for preparing nanoscale reactions using nucleic acids are presented. Nucleic acids are captured saturably, yet reversibly, on the internal surface of the reaction chamber, typically a capillary. Excess nucleic acid is removed and the reaction is performed directly within the capillary. Alternatively, the saturably bound nucleic acid is eluted, dispensing a metered amount of nucleic acid for subsequent reaction in a sep. chamber. Devices for effecting the methods of the invention and a system designed advantageously to utilize the methods for high throughput

nucleic acid sequencing reactions using capillary array electrophoresis are also provided.

IC ICM C12Q001-68

CC 9-1 (Biochemical Methods)

Section cross-reference(s): 3, 6

IT Nucleotides, uses

RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
 (2',3'-dideoxyribo-, triphosphates; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)

IT Archaeobacteria (Archaea)

Bacteriophage

Eukaryote (Eukaryotae)

Plasmid vectors

Plasmids

Prokaryote

Virus
 (DNA isolated from; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)

IT Primers (nucleic acid)

RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
 (DNA, Dye-labeled; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)

IT Halides

RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
 (Tetraamine, for immobilizing DNA templet; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)

IT Apparatus
 (air-based thermal cycling; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)

IT Genetic polymorphism
 (amplified fragment length polymorphism; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)

IT Capillary electrophoresis
 (array; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)

IT Biotechnology
 (biochips, containing capillary array; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)

IT Glass, biological studies

Metals, biological studies

Semimetals

RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
 (channel; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)

IT Denaturants

- (chaotropic, for immobilizing DNA templet; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)
- IT DNA formation
(chemical or enzymic; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)
- IT Thermal cycling
(device for preparing nucleic acid templet; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)
- IT Microsatellite DNA
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(devices for anal. of; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)
- IT **Genotyping** (method)
(devices for; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)
- IT Fluorescent substances
(dideoxynucleotide triphosphates or primer conjugated with; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction)
- IT DNA
RL: ANT (Analyte); ANST (Analytical study)
(double-stranded; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)
- IT PCR (polymerase chain reaction)
(for preparing nucleic acid templet; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)
- IT DNA
RL: ANT (Analyte); BPN (Biosynthetic preparation); ANST (Analytical study); BIOL (Biological study); PREP (Preparation)
(immobilized; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)
- IT Capillary tubes
Nanotubes
(methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)
- IT DNA
Nucleic acids
RL: ANT (Analyte); ANST (Analytical study)
(methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)
- IT Deoxyribonucleoside triphosphates
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)
- IT Oligonucleotides
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(methods and apparatus for nanoscale nucleic acid template capture and

- normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)
- IT RNA
 RL: ANT (Analyte); ANST (Analytical study)
 (mol. weight distribution of; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)
- IT Molecular weight distribution
 (of DNA; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)
- IT DNA
 RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
 (primer, Dye-labeled; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)
- IT DNA microarray technology
 (sequencing from; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)
- IT DNA
 RL: ANT (Analyte); ANST (Analytical study)
 (single-stranded; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)
- IT DNA sequence analysis
 (submicroliter; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)
- IT 64-17-5, Ethanol, biological studies
 RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
 (70%, for washing DNA; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)
- IT 50-01-1, Guanidinehydrochloride 56-34-8, Tetraethylammonium chloride 57-13-6, Urea, biological studies 67-68-5, Dimethylsulfoxide, biological studies 333-20-0, Potassiumthiocyanate 540-72-7, Sodium thiocyanate 593-84-0, Guanidine thiocyanate 650-51-1, Sodium trichloroacetate 7447-41-8, Lithiumchloride, biological studies 7601-89-0, Sodium perchlorate 7647-15-6, Sodium bromide, biological studies 7681-11-0, Potassium iodide, biological studies 7681-82-5, Sodium iodide, biological studies 7758-02-3, Potassium bromide, biological studies 7778-74-7, Potassium perchlorate 16586-14-4, Potassium trichloroacetate
 RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
 (for immobilizing DNA templet; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)
- IT 9013-05-2, Phosphatase 9014-24-8, RNA polymerase 9031-44-1, Kinase 9031-56-5, Ligase 9032-92-2, Glycosidase 9033-25-4, Methylase 9055-11-2, Endonuclease 9068-38-6, Reverse transcriptase 9075-08-5, Restriction enzyme 37228-74-3, Exonuclease 80449-01-0, Topoisomerase
 RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
 (for preparing DNA templets; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)

electrophoresis)
IT 9012-90-2, DNAPolymerase
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(thermostable, for preparing DNA templates; methods and apparatus for nanoscale
nucleic acid template capture and **normalization** for
submicroliter reaction and uses in submicroliter DNA sequencing for
capillary array electrophoresis)

L95 ANSWER 9 OF 31 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2002:232114 CAPLUS
DOCUMENT NUMBER: 137:211507
TITLE: Evaluation of **normalization** procedures for
oligonucleotide array data based on spiked cRNA
controls
AUTHOR(S): Hill, Andrew A.; Brown, Eugene L.; Whitley, Maryann
Z.; Tucker-Kellogg, Greg; Hunter, Craig P.; Slonim,
Donna K.
CORPORATE SOURCE: Department of Genomics, Genetics Institute/Wyeth-
ayerst Research, Cambridge, MA, 02140, USA
SOURCE: GenomeBiology [online computer file] (2001), 2(12), No
pp. given
CODEN: GNBFW; ISSN: 1465-6914
URL: <http://genomebiology.com/2001/2/12/research/0055>
PUBLISHER: BioMed Central Ltd.
DOCUMENT TYPE: Journal; (online computer file)
LANGUAGE: English
ED Entered STN: 27 Mar 2002
AB Background: Affymetrix oligonucleotide arrays simultaneously measure the
abundances of thousands of mRNAs in biol. samples. Comparability of array
results is necessary for the creation of large-scale gene expression
databases. The standard strategy for normalizing oligonucleotide array
readouts has practical drawbacks. We describe alternative normalization
procedures for oligonucleotide arrays based on a common pool of known
biotin-labeled cRNAs spiked into each hybridization. Results: We first
explore the conditions for validity of the 'constant mean assumption', the
key assumption underlying current normalization methods. We introduce
'frequency normalization', a 'spike-in'-based normalization method which
ests. array sensitivity, reduces background noise and allows comparison
between array designs. This approach does not rely on the constant mean
assumption and so can be effective in conditions where standard procedures
fail. We also define 'scaled frequency', a hybrid normalization method
relying on both spiked transcripts and the constant mean assumption while
maintaining all other advantages of frequency normalization. We compare
these two procedures to a standard global normalization method using exptl.
data. We also use simulated data to estimate accuracy and investigate the
effects of noise. We find that scaled frequency is as reproducible and
accurate as global normalization while offering several practical
advantages. Conclusions: Scaled frequency quantitation is a convenient,
reproducible technique that performs as well as global normalization on
serial expts. with the same array design, while offering several addnl.
features. Specifically, the scaled-frequency method enables the
comparison of expression measurements across different array designs,
yields ests. of absolute message abundance in cRNA and dets. the sensitivity
of individual arrays.
CC 3-1 (Biochemical Genetics)
Section cross-reference(s): 9
ST **normalization** procedures oligonucleotide array data spiked cRNA
controls
IT RNA
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES
(Uses)
(complementary; evaluation of **normalization** procedures for

oligonucleotide array data based on spiked cRNA controls)

IT **Genetic methods**
 (frequency **normalization**, a 'spike-in'-based **normalization** which ests. sensitivity, reduces noise and compares array designs; evaluation of **normalization** procedures for oligonucleotide array **data** based on spiked cRNA controls)

IT **Genetic methods**
 (scaled frequency, a hybrid **normalization** method relying on spiked transcripts and constant mean assumption; evaluation of **normalization** procedures for oligonucleotide array **data** based on spiked cRNA controls)

IT mRNA
 RL: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
 (scaled-frequency method enables measurements across different array designs, ests. of mRNA abundance and dets. sensitivity; evaluation of **normalization** procedures for oligonucleotide array data based on spiked cRNA controls)

IT **Genetic methods**
 (standard global, comparison of frequency **normalization** and scaled frequency **normalization** with standard global **normalization**; evaluation of **normalization** procedures for oligonucleotide array **data** based on spiked cRNA controls)

REFERENCE COUNT: 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> => d 195 iall 10-25; d all 195 26;d iall 27-31 195

L95 ANSWER 10 OF 31 JICST-EPlus COPYRIGHT 2005 JST on STN

ACCESSION NUMBER: 1040787618 JICST-EPlus

TITLE: Genetic Method for Floorplan by O-Tree in Consideration of the Initial Solution

AUTHOR: NUMAYAMA KIMIHIKO; ASAI HIDEKI
 NINOMIYA HIROSHI

CORPORATE SOURCE: Shizuoka Univ., Fac. Engineering, JPN
 Shonan Inst. Technol., Fac. Engineering, JPN

SOURCE: Denshi Joho Tsushin Gakkai Gijutsu Kenkyu Hokoku (IEIC Technical Report (Institute of Electronics, Information and Communication Engineers)), (2004) vol. 104, no. 295(NLP2004 40-53), pp. 7-12. Journal Code: S0532B (Fig. 7, Tbl. 3, Ref. 8)
 ISSN: 0913-5685

PUB. COUNTRY: Japan

DOCUMENT TYPE: Journal; Short Communication

LANGUAGE: Japanese

STATUS: New

ABSTRACT:
 This report describes the **Genetic** Algorithm for solving the non-slicing structure floorplan problem using Tree representation. Furthermore, we propose the method to generate initial solutions of Tree representation using the **Delaunay Triangulation**. Finally, we demonstrate the validity of the proposed method for MCNC benchmark tests through the computer simulations. (author abst.)

CLASSIFICATION: JE10000A; NC03161C (681.3:658.51; 621.3.049.77)

CONTROLLED TERM: VLSI; layout; floor plan; circuit design; tree structure; genetic algorithm; decomposition method; computer simulation

BROADER TERM: LSI; integrated circuit; micro circuit; micro circuit

technique; technology; design; structure; optimization
method; computer application; utilization; simulation

L95 ANSWER 11 OF 31 JICST-EPlus COPYRIGHT 2005 JST on STN

ACCESSION NUMBER: 1000825187 JICST-EPlus

TITLE: Optimum Design Method and Evaluation of Small Sector
Antenna Using Cylindrical Coordinate GA-ICT.

AUTHOR: MARUYAMA TAMAMI; HONMA NAOKI; HORI TOSHIKAZU

CORPORATE SOURCE: Nippon Telegraph and Telephone Corp. (NTT), Network
Innovation Lab., JPN

SOURCE: Denshi Joho Tsushin Gakkai Gijutsu Kenkyu Hokoku (IEIC
Technical Report (Institute of Electronics, Information and
Communication Engineers)), (2000) vol. 100, no. 200(SAT2000
29-39), pp. 67-74. Journal Code: S0532B (Fig. 10, Ref. 15)

PUB. COUNTRY: Japan

DOCUMENT TYPE: Journal; Article

LANGUAGE: Japanese

STATUS: New

ABSTRACT:

We propose a new method for determining the optimum antenna design by combining a **genetic** algorithm(GA) and Improved circuit theory(ICT). Without having to provide initially the basic structure, the GA-ICT method automatically obtains the desired design requirements such as electrical characteristics, antenna shape, and size utilizing an optimization evaluation function. Since the evaluation function is constructed based on the weights derived from the characteristics, it may become difficult to obtain all design requirements at the same time due to the nonlinear characteristics of each item. To overcome this problem, we introduce a vector evaluation method to GA-ICT that generates in parallel calculations different individual sets. The evaluation functions have different weights to generate different chromosomes that satisfy other design conditions in the first parallel GA operation and the sets are merged in the next GA operation. By applying this vector evaluated GA-ICT to the sector antenna down sizing problem, we were able to downsize the multi-sector monopole Yagi-Uda **array** antenna(MSMPYA) by 70%. (author abst.)

CLASSIFICATION: ND06000M (621.396.67)

CONTROLLED TERM: multi-beam antenna; **genetic** algorithm; optimum
design; antenna design; Yagi-Uda antenna; cylinder;
coordinate system; small type

BROADER TERM: beam antenna; antenna(electric); optimization method;
design; communication design; end-fire **array**
antenna; **array** antenna; linear antenna; hollow
body; solid(cubic); type

L95 ANSWER 12 OF 31 JICST-EPlus COPYRIGHT 2005 JST on STN

ACCESSION NUMBER: 960994917 JICST-EPlus

TITLE: Modeling and Integrated Optimum Design of Structure and
Control System.

AUTHOR: KAJIWARA ITSURO

CORPORATE SOURCE: Tokyo Inst. of Technol.

SOURCE: Nippon Kikai Gakkai Zenkoku Taikai Koen Ronbunshu, (1996)
vol. 74th, no. Vol 5, pp. 82-87. Journal Code: X0587A (Fig.
9, Tbl. 1, Ref. 6)

PUB. COUNTRY: Japan

DOCUMENT TYPE: Conference; Short Communication

LANGUAGE: Japanese

STATUS: New

ABSTRACT:

Approaches for modeling of the system based on modal analysis and integrated optimum design of structure/control system to achieve the high performances concerning the vibration suppression and the high speed positioning are

presented in this paper. In the integrated optimization for the vibration suppression, the structural shape and the sensor/actuator placement are simultaneously optimized based on sensitivity analysis in LQR control system and GA approach in H.INF. control system. In the integrated optimization for the high speed positioning, the desired frequency characteristics of the servosystem are achieved by the integrated optimization of structure and dynamic compensator, and the time history response of the closed-loop system can be improved by the integrated optimization of structure and LQI control system. Application results with simplified models show the effectiveness and the practicability of the proposed approaches. (author abst.)

CLASSIFICATION: IA02030D; HD02000E (681.5.03.015; 624.041/.047)
 CONTROLLED TERM: structure analysis; structure(construction); control system; optimum design; concurrency; **coordinate system**; modeling; vibration control; position control; optimum control; sensor **array**; actuator; sensitivity analysis; optimization method; algorithm; structural system; LQG control; **genetic** algorithm
 BROADER TERM: analysis; system; design; property; operation(processing); control; sensor; instrumentation element; control equipment; equipment

L95 ANSWER 13 OF 31 PASCAL COPYRIGHT 2005 INIST-CNRS. ALL RIGHTS RESERVED.
 on STN DUPLICATE 5

ACCESSION NUMBER: 1998-0307624 PASCAL
 COPYRIGHT NOTICE: Copyright .COPYRGT. 1998 INIST-CNRS. All rights reserved.
 TITLE (IN ENGLISH): Recognising building patterns using matched filters and genetic search
 Extraction of man-made objects from aerial and satellite images
 AUTHOR: CROSS A. D. J.; HANCOCK E. R.
 CORPORATE SOURCE: LEBERL F. (ed.); KALLIANY R. (ed.); GRUBER M. (ed.)
 Department of Computer Science, University of York, York, YO1 5DD, United Kingdom
 Austrian Research Centre Seibersdorf, 2444 Seibersdorf, Austria; Institute for Computer Graphics and Vision, Technical University Graz, Muenzgrabenstrasse 11, 8010 Graz, Austria
 International Association of Pattern Recognition. Technical Committee 7 (TC-7, "Photogrammetry and Remote Sensing", INT (patr.)
 SOURCE: ISPRS journal of photogrammetry and remote sensing, (1998), 53(2), 95-107, 29 refs.
 Conference: IAPR TC-7 Workshop "Mapping Buildings, Roads and Other Man-Made Structures from Images", Graz (Austria), 2 Sep 1996
 Illustrations
 ISSN: 0924-2716
 DOCUMENT TYPE: Journal; Conference
 BIBLIOGRAPHIC LEVEL: Analytic
 COUNTRY: Netherlands
 LANGUAGE: English
 AVAILABILITY: INIST-4647, 354000075809890040
 ABSTRACT: This paper is concerned with recognising buildings in aerial images. We abstract the images in terms of relational graphs. Specifically, we use **Delaunay triangulations** to represent the arrangement of located buildings. Localisation is realised using matched filters. The filters are trained by drawing upon the duality between convolution in the image domain and multiplication in

the Fourier domain. The matched filters prove to be remarkably stable. We match **Delaunay** graphs representing image pairs using **genetic** search with a Bayesian relational consistency criterion as fitness function. The use of **genetic** search allows us to perform the optimisation without the traditional problems of sensitivity to initial conditions and convergence to local optima.

CLASSIFICATION CODE: 225B04
001E01M04; Universe sciences; Earth sciences; Internal geophysics

CONTROLLED TERM: Austria; urban areas; triangulation; buildings; aerial photography; imagery; stereograms; image analysis

BROADER TERM: Central Europe; Europe

L95 ANSWER 14 OF 31 PASCAL COPYRIGHT 2005 INIST-CNRS. ALL RIGHTS RESERVED.
on STN

ACCESSION NUMBER: 2004-0495992 PASCAL

COPYRIGHT NOTICE: Copyright .COPYRG. 2004 INIST-CNRS. All rights reserved.

TITLE (IN ENGLISH): A global optimal registration method for satellite remote sensing images
Programmetric computer vision : Graz, 9-13 September 2002

AUTHOR: GONGJIAN WEN; DEREN LI; LIANGPEI ZHANG; XIUXIAO YUAN
KALLIAN Y. (ed.); LEBERT F. (ed.)

CORPORATE SOURCE: LIESMARS, Wuhan University, Wuhan, Hubei, China; ATR
National Lab National University of Defense
Technology, Changsha, Hunan, China
International Society for Photogrammetry and Remote Sensing, United Kingdom (patr.)

SOURCE: The international archives of the photogrammetry,
remote sensing and spatial information sciences
(Print), (2002), A394-A399, 1 tabl., 8 refs.
Conference: ISPRS Commission III Symposium, Graz
(Austria), 9 Sep 2002
Illustrations; Table
ISSN: 1682-1750

DOCUMENT TYPE: Journal; Conference

BIBLIOGRAPHIC LEVEL: Analytic

COUNTRY: United Kingdom

LANGUAGE: English

AVAILABILITY: INIST-Y 34307, 354000124342140630

ABSTRACT: One of the main obstacles in image registration is the precise estimation of a mapping function that determines geometric transformation between two image **coordinate systems**. For conventional image registration methods, their registration results are not the global optimal, and accuracy is low because only a few local **control points** are used for the estimation. In this paper, we develop a global optimal method in order to get a registration approach with high accuracy. In our method, an energy function that is directly related to the parameters of the mapping function is defined in the whole image. Thus, estimation of the global optimal mapping function can be solved through energy optimization. In defining the energy function, we choose a strength measure that is based on contour edge points. It is demonstrated that the strength measure is insensitive to image radiometric

distortion. Therefore, our method is applicable for various kinds of images, even for different sensors images. In order to solve the energy optimization, we design a pipelining hybrid framework that combines **genetic** algorithms (GAs) and a simplex method (SM). The GAs are applied firstly to look for a few initial guesses from some sub-images, and then the SM is employed to get the optima of the energy function near these initial guesses. It is found that the pipelining hybrid framework is not trapped in a local optimum, and converges fast. Hence, one of the advantages of our algorithm is that it successfully avoids advanced feature extraction and feature matching in the image registration. Its characteristics are of automatic and robust. Experimental results have shown that our method can provide better accuracy than the manual registration.

CLASSIFICATION CODE:

225B04

001E01M04; Universe sciences; Earth sciences; Internal geophysics

CONTROLLED TERM:

imagery; Space remote sensing; methodology; algorithms; cartography; transformations; **coordinate systems**; accuracy; optimization; distortionL95 ANSWER 15 OF 31 PASCAL COPYRIGHT 2005 INIST-CNRS. ALL RIGHTS RESERVED.
on STN

ACCESSION NUMBER: 2001-0063483 PASCAL

COPYRIGHT NOTICE: Copyright .COPYRG. 2001 INIST-CNRS. All rights reserved.

TITLE (IN ENGLISH): Heuristic approach to image registration
Automatic target recognition X : Orlando FL, 26-28 April 2000AUTHOR: GERTNER Izidor; MASLOV Igor
SADJADI Firooz A. (ed.)

CORPORATE SOURCE: Dept. of Computer Science, City College, City Univ. of New York, United States; Dept. of Computer Science, Graduate School and Univ. Center, City Univ. of New York, United States

SOURCE: SPIE proceedings series, (2000), 4050, 238-244, 3 refs.
Conference: 10 Automatic target recognition.
Conference, Orlando FL (United States), 26 Apr 2000
ISSN: 1017-2653
ISBN: 0-8194-3676-3

DOCUMENT TYPE: Journal; Conference

BIBLIOGRAPHIC LEVEL: Analytic

COUNTRY: United States

LANGUAGE: English

AVAILABILITY: INIST-21760, 354000092034160270

ABSTRACT: Image registration, i.e. correct mapping of images obtained from different sensor readings onto common reference frame, is a critical part of multi-sensor ATR/AOR systems based on readings from different types of sensors. In order to fuse two different sensor readings of the same object, the readings have to be put into a common **coordinate system**. This task can be formulated as optimization problem in a space of all possible affine transformations of an image. In this paper, a combination of heuristic methods is explored to register gray-scale images. The modification of **Genetic** Algorithm is used as

the first step in global search for optimal transformation. It covers the entire search space with (randomly or heuristically) scattered probe points and helps significantly reduce the search space to a subspace of potentially most successful transformations. Due to its discrete character, however, Genetic Algorithm in general can not converge while coming close to the optimum. Its termination point can be specified either as some predefined number of generations or as achievement of a certain acceptable convergence level. To refine the search, potential optimal subspaces are searched using more delicate and efficient for local search Taboo and Simulated Annealing methods.

CLASSIFICATION CODE:

001B00G07D; Physics; Metrology
001D04A05C; Applied sciences; Information theory,
Signal processing

PHYS. AND ASTRONOM.CODE: 0707D

CONTROLLED TERM:

Image registration; Multisensor; **Coordinate system**; Measurement sensor; Sensor **array**; Affine transformation; Heuristic approach; Image recognition; Algorithms; Image matching; Total attenuated reflection; Infrared spectroscopy; Theoretical study

L95 ANSWER 16 OF 31 Elsevier BIOBASE COPYRIGHT 2005 Elsevier Science B.V.
on STN DUPLICATE

ACCESSION NUMBER:

2004199365 ESBIOWASE

TITLE:

Geographic patterns of (genetic, morphologic, linguistic) variation: How barriers can be detected by using Monmonier's algorithm

AUTHOR:

Manni F.; Guerard E.; Heyer E.

CORPORATE SOURCE:

F. Manni, Dept. Hommes, Natures, Societes, Human Population Genetics Group, CNRS UMR 5145, 17 Place du Trocadero, Paris, France.

SOURCE:

Human Biology, (2004), 76/2 (173-190), 35 reference(s)
CODEN: HUBIAA ISSN: 0018-7143

DOCUMENT TYPE:

Journal; Article

COUNTRY:

United States

LANGUAGE:

English

SUMMARY LANGUAGE:

English

ABSTRACT:

When sampling locations are known, the association between genetic and geographic distances can be tested by spatial autocorrelation or regression methods. These tests give some clues to the possible shape of the genetic landscape. Nevertheless, correlation analyses fail when attempting to identify where genetic barriers exist, namely, the areas where a given variable shows an abrupt rate of change. To this end, a computational geometry approach is more suitable because it provides the locations and the directions of barriers and because it can show where geographic patterns of two or more variables are similar. In this frame we have implemented Monmonier's (1973) maximum difference algorithm in a new software package to identify genetic barriers. To provide a more realistic representation of the barriers in a genetic landscape, we implemented in the software a significance test by means of bootstrap matrices analysis. As a result, the noise associated with genetic markers can be visualized on a geographic map and the areas where genetic barriers are more robust

can be identified. Moreover, this multiple matrices approach can visualize the patterns of variation associated with different markers in the same overall picture. This improved Monmonier's method is highly reliable and can be applied to nongenetic data whenever sampling locations and a distance matrix between corresponding data are available.

CLASSIFICATION CODE:

99 General

SUPPLEMENTARY TERM:

Genetic barriers; Monmonier's algorithm;
Delaunay triangulation; Bootstrap
analysis; Gene geophy; **Genetic** structures

L95 ANSWER 17 OF 31

INSPEC (C) 2005 IEE on STN

DUPLICATE 2

ACCESSION NUMBER:

2003:7697571 INSPEC

DOCUMENT NUMBER:

C2003-09-4260-012

TITLE:

Mesh optimization for surface approximation using an
efficient coarse-to-fine evolutionary algorithm.

AUTHOR:

Hui-Ling Huang; Shinn-Ying Ho (Dept. of Inf. Eng.,
Feng Chia Univ., Taichung, Taiwan)

SOURCE:

Pattern Recognition (May 2003) vol.36, no.5,
p.1065-81. 24 refs.

Doc. No.: S0031-3203(02)00113-9

Published by: Elsevier

Price: CCCC 0031-3203/03/\$30.00

CODEN: PTNRA8 ISSN: 0031-3203

SICI: 0031-3203(200305)36:5L:1065:MOSA;1-8

DOCUMENT TYPE:

Journal

TREATMENT CODE:

Theoretical

COUNTRY:

United Kingdom

LANGUAGE:

English

ABSTRACT:

The investigated mesh optimization problem $C(N, n)$ for surface approximation, which is NP-hard, is to minimize the global error between a digital surface and its approximating mesh surface by efficiently locating a limited number n of grid points which are a subset of the original N sample points. This paper proposes an efficient coarse-to-fine evolutionary algorithm (CTFEA) with a novel orthogonal **array** crossover (OAX) for solving the mesh optimization problem. OAX adaptively divides the meshes of parents into a number of parts using a tuning parameter for applying a coarse-to-fine technique. Meshes of children are formed from an intelligent combination of the good parts from their parents rather than the conventional random combination. The better one of two parts in two parents is chosen by evaluating the contribution of the individual parts to the fitness function based on orthogonal experimental design. The coarse-to-fine technique of CTFEA can advantageously solve large mesh optimization problems. Furthermore, CTFEA using an additional inheritance technique can further efficiently locate the grid points in the mesh surface. It is shown empirically that CTFEA outperforms the existing evolutionary algorithm in terms of both approximation quality and convergence speed, especially in solving large mesh optimization problems.

CLASSIFICATION CODE:

C4260 Computational geometry; C4130 Interpolation and
function approximation (numerical analysis); C6130B
Graphics techniques

CONTROLLED TERM:

EVOLUTIONARY COMPUTATION; **GENETIC**

SUPPLEMENTARY TERM: ALGORITHMS; MESH GENERATION; SURFACE FITTING
mesh optimization; NP-hard; **orthogonal array**
crossover; tuning parameter; **Delaunay**
triangulation; evolutionary computation; CTFEA;
inheritance; **genetic algorithm**; surface
approximation

L95 ANSWER 18 OF 31 INSPEC (C) 2005 IEE on STN DUPLICATE 3
ACCESSION NUMBER: 2001:7046174 INSPEC
DOCUMENT NUMBER: C2001-11-4260-018
TITLE: Multicriteria-optimized triangulations.
AUTHOR: Kolingerova, I. (Dept. of Comput. Sci. & Eng., Univ.
of West Bohemia, Czech Republic); Ferko, A.
SOURCE: Visual Computer (Aug. 2001) vol.17, no.6, p.380-95. 47
refs.
Published by: Springer-Verlag
CODEN: VICOE5 ISSN: 0178-2789
SICI: 0178-2789(200108)17:6L:380:MOT;1-1
DOCUMENT TYPE: Journal
TREATMENT CODE: Practical; Theoretical
COUNTRY: Germany, Federal Republic of
LANGUAGE: English
ABSTRACT: Triangulation of a given set of points in a plane is
one of the most commonly solved problems in computer
graphics and computational geometry. Because they are
useful in many applications, triangulations must
provide well-shaped triangles. Many criteria have been
developed to provide such meshes, including weight and
angular criteria. Each criterion has its pros and
cons, some of them are difficult to compute, and
sometimes a polynomial algorithm is not even known. By
any of the existing deterministic methods, it is not
possible to compute a triangulation which satisfies
more than one criterion or which contains parts
developed according to several criteria. We explain
how such a mixture can be generated using genetic
optimization.
CLASSIFICATION CODE: C4260 Computational geometry; C6130B Graphics
techniques; C4185 Finite element analysis; C1180
Optimisation techniques
CONTROLLED TERM: COMPUTATIONAL GEOMETRY; COMPUTER GRAPHICS; GENETIC
ALGORITHMS; MESH GENERATION
SUPPLEMENTARY TERM: **multicriteria-optimized triangulations**;
computer graphics; computational geometry; well-shaped
triangles; meshes; weight criteria; angular criteria;
polynomial algorithm; deterministic methods;
genetic optimization; **minimum-weight**
triangulation; **Delaunay triangulation**

L95 ANSWER 19 OF 31 INSPEC (C) 2005 IEE on STN DUPLICATE 4
ACCESSION NUMBER: 1998:6050414 INSPEC
DOCUMENT NUMBER: B9811-8380-011; C9811-7410B-093
TITLE: Optimal design of linear oscillatory actuator using
genetic algorithm.
AUTHOR: Enomoto, H.; Harada, K.; Ishihara, Y.; Todaka, T.
(Dept. of Electr. Eng., Doshisha Univ., Kyoto, Japan);
Hirata, K.
SOURCE: IEEE Transactions on Magnetics (Sept. 1998) vol.34,
no.5, pt.1, p.3515-18. 5 refs.
Published by: IEEE
Price: CCCC 0018-9464/98/\$10.00
CODEN: IEMGAQ ISSN: 0018-9464

SICI: 0018-9464(199809)34:5:1L.3515:ODLO;1-M
 Conference: 11th International Conference on
 Computation of Electromagnetic Fields (COMPUMAG). Rio
 de Janeiro, Brazil, 3-6 Nov 1997

DOCUMENT TYPE: Conference Article; Journal
 TREATMENT CODE: Theoretical
 COUNTRY: United States
 LANGUAGE: English
 ABSTRACT: This paper presents the optimal design method of a
 linear oscillatory actuator (LOA) using the
genetic algorithm (GA). In this method, the GA
 is coupled with a 2D-dynamic analysis code based on
 the finite element method (FEM) to obtain the optimal
 geometry which can give a satisfactory dynamic
 performance. In order to take the motion of the LOA
 into consideration, the finite element meshes are
 automatically regenerated using **Delaunay**
triangulation. The utility of this method is
 verified through the comparison of the performances of
 the optimal geometry and those of the initial
 geometry.

CLASSIFICATION CODE: B8380 Control gear and apparatus; B8330 Linear
 machines; B0260 Optimisation techniques; B0290T Finite
 element analysis; C7410B Power engineering computing;
 C4185 Finite element analysis; C4260 Computational
 geometry

CONTROLLED TERM: ELECTRIC ACTUATORS; ELECTRIC MACHINE CAD; GENETIC
 ALGORITHMS; LINEAR MOTORS; MESH GENERATION

SUPPLEMENTARY TERM: linear oscillatory actuator; design optimisation;
genetic algorithm; GA; 2D-dynamic analysis
 code; finite element method; FEM; optimal geometry;
 dynamic performance; **Delaunay triangulation**;
 CPU time

ELEMENT TERM: D

L95 ANSWER 20 OF 31 INSPEC (C) 2005 IEE on STN DUPLICATE 7
 ACCESSION NUMBER: 1993:4360675 INSPEC
 DOCUMENT NUMBER: A9308-9650M-001
 TITLE: A spectral analysis of ordinary chondrites, S-type
 asteroids, and their component minerals:
genetic implications.

AUTHOR: Fanale, F.P.; Clark, B.E.; Bell, J.F. (Dept. of Geol.
 & Geophys., Sch. of Ocean & Earth Sci. & Technol.,
 Hawaii Univ., Honolulu, HI, USA)

SOURCE: Journal of Geophysical Research (25 Dec. 1992) vol.97,
 no.E12, p.20863-74. 75 refs.
 Price: CCCC 0148-0227/92/92JE-02228\$05.00
 CODEN: JGREAA2 ISSN: 0148-0227

DOCUMENT TYPE: Journal
 TREATMENT CODE: Bibliography; Experimental
 COUNTRY: United States
 LANGUAGE: English
 ABSTRACT: Three salient features of visible and infrared
 reflectance spectra of ordinary chondrites (OCs) and
 S-type asteroids are albedo at 0.56 μ m; continuum
 slope; and depth of the electronic absorption band due
 to octahedrally coordinated Fe²⁺ in olivine and
 pyroxene. These quantities were numerically extracted
 from the spectra of 23 OCs and 39 S-type asteroids to
 be plotted in a three-dimensional **coordinate**
system. When the region containing the 39
 S-asteroid spectra is compared with that of the

altered and unaltered OCs, it is found that not one of the OCs falls within the S-asteroid region. The range of S-asteroid parameters is then compared with potential pure 'end-member' components most likely to result from magmatic differentiation of a chondritic protoasteroid: olivine, orthopyroxene, clinopyroxene, and Fe,Ni meteorite metal. The S-asteroid

array is consistent with random mixtures of

the differentiated components. The S-asteroids may supply achondrites, irons, and stony irons to Earth rather than well-mixed breccias of these components. A9650M Meteorites, micrometeorites; A9630H Asteroids; A9635E Chemical composition; A9580J Photographic region; A9580G Infrared

CLASSIFICATION CODE:

CONTROLLED TERM:

ALBEDO; ASTEROIDS; ASTRONOMICAL SPECTRA; INFRARED ASTRONOMICAL OBSERVATIONS; METEORITES; MINERALS; VISIBLE ASTRONOMICAL OBSERVATIONS

SUPPLEMENTARY TERM:

stony meteorites; asteroid-meteorite connection; differentiated mineral components mixture; near-IR; metallic component spectrum; 560-nm albedo; near-UV; absorption band depth; stony-Fe meteorites; small chondritic asteroids metamorphism; EM induction heating; asteroids heating; spectral analysis; ordinary chondrites; S-type asteroids; component minerals; visible; infrared reflectance spectra; continuum slope; electronic absorption band; olivine; pyroxene; **three-dimensional coordinate system**

; magmatic differentiation; chondritic protoasteroid; orthopyroxene; clinopyroxene; achondrites; stony irons; 300 to 2500 nm; 560 nm; octahedrally coordinated Fe²⁺; Fe-Ni meteorite metal; FeMgSiO₄; FeMgSiO₃; Fe meteorites; 26Al decay heating FeNi bin, Fe bin, Ni bin; FeMgSiO₄ ss, SiO₄ ss, Fe ss, Mg ss, O₄ ss, Si ss, O ss; FeMgSiO₃ ss, Fe ss, Mg ss, O₃ ss, Si ss, O ss; Fe el; Al el; Fe el wavelength 3.0E-07 to 2.5E-06 m; wavelength 5.6E-07 m S; Cs*O; OCs; O cp; cp; Cs cp; Fe; Fe²⁺; Fe ip 2; ip 2; 23OCs; is; O is; 23O; 39S; S is; Ni; Fe*Ni; Fe sy 2; sy 2; Ni sy 2; Fe-Ni; Fe*Mg*O*Si; Fe sy 4; sy 4; Mg sy 4; O sy 4; Si sy 4; FeMgSiO₄; Fe cp; Mg cp; Si cp; FeMgSiO₃; Al; 26Al; Al is; FeNi; Ni cp; FeMgSiO; O*Si; SiO; Mg; O; Si

CHEMICAL INDEXING:

PHYSICAL PROPERTIES:

ELEMENT TERM:

L95 ANSWER 21 OF 31 INSPEC (C) 2005 IEE on STN

ACCESSION NUMBER: 2004:8248174 INSPEC

DOCUMENT NUMBER: C2005-03-1180-002

TITLE: An improved genetic algorithm to solve the Euclidean plane TSP by using geometry structure.

AUTHOR: Pan Liang; Zhu Hua-yong; Shen Lin-cheng; Chang Wen-sen (Coll. of Mechatronics Eng. & Autom., National Univ. of Defense Technol., Changsha, China)

SOURCE: Journal of National University of Defense Technology (Oct. 2004) vol.26, no.5, p.109-14. 21 refs. Published by: Editorial Department J. Natl. Univ. Def. Technol

CODEN: GKDXEM ISSN: 1001-2486

SICI: 1001-2486(200410)26:5L:109:IGAS;1-E

DOCUMENT TYPE: Journal

TREATMENT CODE: Theoretical; Experimental

COUNTRY: China

LANGUAGE: Chinese

ABSTRACT: The TSP is a classic combinatorial optimization

problem. According to the character of the optimal tour of Euclidean plane TSP problem, the sub-path and related notions are presented. A tour construction algorithm is designed by using convex hull, and a **genetic** algorithm is improved to solve the problem by using **Delaunay triangulation** diagram as heuristic information. The experimental results in the 144 cities in China and other TSP instances show that the algorithm is effective.

CLASSIFICATION CODE:

C1180 Optimisation techniques; C4260 Computational geometry; C4185 Finite element analysis

CONTROLLED TERM:

GENETIC ALGORITHMS; MESH GENERATION

SUPPLEMENTARY TERM:

improved genetic algorithm; Euclidean plane TSP; geometry structure; combinatorial optimization problem; tour construction algorithm; convex hull; **Delaunay triangulation diagram**; heuristic information; China; traveling salesman problem

L95 ANSWER 22 OF 31 INSPEC (C) 2005 IEE on STN

ACCESSION NUMBER:

2003:7790823 INSPEC

DOCUMENT NUMBER:

B2004-01-6135-042; C2004-01-5260B-038

TITLE:

Extraction of outlines in arbitrary shape from binary images using genetic algorithm.

AUTHOR:

Abe, M.; Ouchi, T.; Kawamata, M. (Graduate Sch. of Eng., Tohoku Univ., Sendai, Japan)

SOURCE:

Transactions of the Institute of Electronics, Information and Communication Engineers D-II (July 2003) vol.J86D-II, no.7, p.1036-48. 12 refs.
Published by: Inst. Electron. Inf. & Commun. Eng
CODEN: DTGDE7 ISSN: 0915-1923
SICI: 0915-1923(200307)J86DII:7L.1036:EOAS;1-4

DOCUMENT TYPE:

Journal

TREATMENT CODE:

Practical; Theoretical

COUNTRY:

Japan

LANGUAGE:

Japanese

ABSTRACT:

This paper proposes a method to extract outlines in arbitrary shapes from images using **genetic** algorithm (GA). The target images are binary images including disconnected outlines and noise. The proposed method can extract outlines recognized by human visual ability. In this method, **Delaunay triangulation** is first used to obtain a graph including the outline. Second, vertices and edges locally recognized as noise in the graph are eliminated. Finally, from the graph for which noise has been reduced, the outlines is extracted using GA, where the polygons in the graph are coded into chromosomes. Experimental results show that the proposed method can extract an outline of arbitrary shape from the image. Moreover, the proposed method is extended to extract multiple outlines. Experimental results also show the extended method can extract all outlines in the image.

CLASSIFICATION CODE:

B6135 Optical, image and video signal processing; B0260 Optimisation techniques; C5260B Computer vision and image processing techniques; C1180 Optimisation techniques; C1250M Image recognition; C4260 Computational geometry

CONTROLLED TERM:

EDGE DETECTION; FEATURE EXTRACTION; GENETIC ALGORITHMS; IMAGE DENOISING; MESH GENERATION

SUPPLEMENTARY TERM:

arbitrary shape; binary image; **genetic**

algorithm; disconnected outline; human visual ability; **Delaunay triangulation**; noise elimination; outline extraction

L95 ANSWER 23 OF 31 INSPEC (C) 2005 IEE on STN
ACCESSION NUMBER: 2003:7547323 INSPEC
DOCUMENT NUMBER: B2003-04-6135E-042; C2003-04-1250M-048
TITLE: Extraction of outlines in arbitrary shape using genetic algorithm.
AUTHOR: Ouchi, T.; Abe, M.; Kawamata, M.
SOURCE: Record of Electrical and Communication Engineering
Conversazione Tohoku University (Oct. 2002) vol.71, no.1, p.421-2. 6 refs.
Published by: Tohoku Univ
CODEN: TDDDAI ISSN: 0385-7719
SICI: 0385-7719(200210)71:1L.421:EOAS;1-3
DOCUMENT TYPE: Journal
TREATMENT CODE: Theoretical; Experimental
COUNTRY: Japan
LANGUAGE: Japanese
ABSTRACT: This paper proposes a method to extract outlines in arbitrary shape from images using a **Genetic Algorithm (GA)**. The target images are binary images including disconnected outlines and noise. The proposed method can extract outlines recognized by human visual ability. In this method, **Delaunay triangulation** is first used to obtain a graph including the outline. Second, vertexes and edges locally recognized as noise in the graph are eliminated. Finally, from the graph of which the noise has been reduced, the outline is extracted using GA, where the polygons in the graph are coded into chromosomes. Experimental results show that the proposed method can extract an outline of arbitrary shape from the image. Moreover, the proposed method is extended to extract multiple outlines. Experimental results also show that the extended method can extract all outlines in the image.
CLASSIFICATION CODE: B6135E Image recognition; B0260 Optimisation techniques; C1250M Image recognition; C1180 Optimisation techniques; C5260B Computer vision and image processing techniques
CONTROLLED TERM: FEATURE EXTRACTION; GENETIC ALGORITHMS; GRAPH THEORY; IMAGE RECOGNITION
SUPPLEMENTARY TERM: arbitrary shape outlines; outline extraction; multiple outlines; image processing; **genetic algorithm**; binary images; disconnected outlines; noise; **Delaunay triangulation**; graph; polygon coding; chromosomes

L95 ANSWER 24 OF 31 INSPEC (C) 2005 IEE on STN
ACCESSION NUMBER: 1997:5573108 INSPEC
DOCUMENT NUMBER: C9706-4260-065
TITLE: A genetic algorithm for the minimum weight triangulation.
AUTHOR: Kaihuai Qin; Wenping Wang (Dept. of Comput. Sci., Hong Kong Univ., Hong Kong); Minglun Gong
SOURCE: Proceedings of 1997 IEEE International Conference on Evolutionary Computation (ICEC '97) (Cat. No.97TH8283) New York, NY, USA: IEEE, 1997. p.541-6 of xv+724 pp. 17 refs.
Conference: Indianapolis, IN, USA, 13-16 April 1997

Sponsor(s): IEEE; IEEE Neural Network Council (NNC);
 Evolutionary Computation (ICEC '97)
 Price: CCCC 0 7803 3949 5/97/\$10.00
 ISBN: 0-7803-3949-5

DOCUMENT TYPE: Conference Article
 TREATMENT CODE: Theoretical
 COUNTRY: United States
 LANGUAGE: English

ABSTRACT: In this paper, a new method for the minimum weight triangulation of points on a plane, called genetic minimum weight triangulation (GMWT), is presented based on the rationale of genetic algorithms. Polygon crossover and its algorithm for triangulations are proposed. New adaptive genetic operators, or adaptive crossover and mutation operators, are introduced. It is shown that the new method for the minimum weight triangulation can obtain more optimal results of triangulations than the greedy algorithm.

CLASSIFICATION CODE: C4260 Computational geometry; C1180 Optimisation techniques; C4185 Finite element analysis

CONTROLLED TERM: COMPUTATIONAL GEOMETRY; GENETIC ALGORITHMS; MESH GENERATION

SUPPLEMENTARY TERM: **genetic algorithm; GMWT; genetic minimum weight triangulation; polygon crossover; adaptive genetic operators; adaptive crossover; mutation operators; greedy algorithm; Delaunay triangulation**

L95 ANSWER 25 OF 31 INSPEC (C) 2005 IEE on STN

ACCESSION NUMBER: 1994:4834992 INSPEC
 DOCUMENT NUMBER: B9501-6140C-218; C9501-5260B-121

TITLE: A **genetic** algorithm approach to camera calibration in 3D machine vision.

AUTHOR: Roberts, M.; Naftel, A.J. (Dept. of Math. & Stat., Central Lancashire Univ., Preston, UK)

SOURCE: IEE Colloquium on 'Genetic Algorithms in Image Processing and Vision' (Digest No.1994/193)
 London, UK: IEE, 1994. p.12/1-5 of 78 pp. 13 refs.
 Conference: London, UK, 20 Oct 1994
 Sponsor(s): IEE

DOCUMENT TYPE: Conference Article
 TREATMENT CODE: Theoretical
 COUNTRY: United Kingdom
 LANGUAGE: English

ABSTRACT: The camera calibration problem in 3D machine vision involves the determination of the interior orientation (internal camera geometry) and exterior orientation parameters (position and angular rotation relative to a specified 3D world **coordinate system**) using known **control points**. Additional parameters can be used to model the nonlinear effects of lens distortion. If an unknown targeted point is then imaged in two cameras or single camera together with an active structured light source (e.g. a projector), the position of the object point can be determined by intersecting the two calibrated rays.

CLASSIFICATION CODE: B6140C Optical information, image and video signal processing; B7130 Measurement standards and calibration; B0260 Optimisation techniques; C5260B Computer vision and image processing techniques; C1180 Optimisation techniques

CONTROLLED TERM: CALIBRATION; COMPUTER VISION; **GENETIC**
 ALGORITHMS; STEREO IMAGE PROCESSING
 SUPPLEMENTARY TERM: 3D machine vision; camera calibration; **genetic**
algorithm; interior orientation; internal camera
 geometry; exterior orientation; position; angular
 rotation; lens distortion nonlinear effects; active
 structured light source
 ELEMENT TERM: D

L95 ANSWER 26 OF 31 COMPUSCIENCE COPYRIGHT 2005 FIZ KARLSRUHE on STN
 DUPLICATE 6
 AN 1998(3):MA59507 COMPUSCIENCE
 TI Optimal tetrahedral mesh generation for three-dimensional point set.
 AU Qin, Kaihuai; Wu, Bian; Guan, Youjiang; Ge, Zhenzhou
 SO Sci. China, Ser. E. (1997) v. 40(2) p. 135-143.
 1997.
 DT Journal
 TC Theoretical
 CY Germany, Federal Republic of
 LA English
 IP FIZKA
 DN 881.68126
 AB Three-dimensional (3D) **triangulation** is a basic topic in
 computer graphics. It is considered very difficult to obtain the global
 optimal 3D **triangulation**, such as the **triangulation**
 which satisfies the max-min solid angle criterion. A new method called
genetic tetrahedral mesh generation algorithm (GTMGA for short)
 is presented. GTMGA is based on the principle of **genetic**
 algorithm and aims at the global optimal **triangulation**. With a
 multiobjective fitness function, GTMGA is able to perform optimizations
 for different requirements. New crossover operator and mutation operator,
 polyhedron crossover and polyhedron mutation, are used in GTMGA. It is
 shown by the experimental results that GTMGA works better than both the
 3D **Delaunay triangulation** and the algorithm based on
 local transformations. (Summary)
 CC *I.3.5 Computational geometry and object modeling
 ST computer graphics; Delaunay triangulation.

L95 ANSWER 27 OF 31 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
 ACCESSION NUMBER: 2004-635295 [61] WPIDS
 DOC. NO. NON-CPI: N2004-502124
 TITLE: Helical conebeam computed tomography imaging system
 performs exact reconstruction of conebeam data projected
 from native scan coordinates of x-ray detector
array, into image representation.
 DERWENT CLASS: S03 S05 T01
 INVENTOR(S): BROWN, K M; HEUSCHER, D J; NOO, F N; PACK, J D
 PATENT ASSIGNEE(S): (PHIG) KONINK PHILIPS ELECTRONICS NV
 COUNTRY COUNT: 108
 PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG	MAIN	IPC
-----------	------	------	------	----	----	------	-----

WO 2004072905	A1	20040826	(200461)*	EN	36	G06T011-00	
---------------	----	----------	-----------	----	----	------------	--

RW:	AT	BE	BG	BW	CH	CY	CZ	DE	DK	EA	EE	ES	FI	FR	GB	GH	GM	GR	HU	IE	IT	KE
	LS	LU	MC	MW	MZ	NL	OA	PT	RO	SD	SE	SI	SK	SL	SZ	TR	TZ	UG	ZM	ZW		

W: AE AG AL AM AT AU AZ BA BB BG BR BW BY BZ CA CH CN CO CR CU CZ DE
 DK DM DZ EC EE EG ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG
 KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NA NI NO NZ
 OM PG PH PL PT RO RU SC SD SE SG SK SL SY TJ TM TN TR TT TZ UA UG
 US UZ VC VN YU ZA ZM ZW

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2004072905	A1	WO 2004-IB386	20040209

PRIORITY APPLN. INFO: US 2003-482380P 20030625; US
 2003-447426P 20030214

INT. PATENT CLASSIF.:

MAIN: G06T011-00

BASIC ABSTRACT:

WO2004072905 A UPAB: 20040923

NOVELTY - An X-ray source (12) arranged transversely to a helical trajectory, produces X-ray conebeam and directs it to the examination region. A X-ray detector **array** (14) detects conebeam from the examination region, and generates projection data in its nature scan coordinates. Several processors perform an exact reconstruction of the conebeam projection data from native scan coordinates, into an image representation.

DETAILED DESCRIPTION - An INDEPENDENT CLAIM is also included for reconstruction method for reconstructing conebeam computed tomography.

USE - Helical conebeam computed tomography imaging system.

ADVANTAGE - Fast and exact image reconstruction of conebeam imaging data is performed, by simplified image reconstruction computations by **transforming** tomographic **projection** data to detector independent voxel based **coordinate system**.

DESCRIPTION OF DRAWING(S) - The figure shows a helical conebeam computed tomography imaging system including exact reconstruction of acquired conebeam projection data.

X-ray source 12
 examination region 14
 X-detector **array** 16
 back projector 42,82
 derivative processor 60
 convolution processor 64

Dwg.1/6

FILE SEGMENT: EPI
 FIELD AVAILABILITY: AB; GI
 MANUAL CODES: EPI: S03-E06B3; S05-D02A1; S05-D02A5E; T01-J06A;
 T01-J10C4B

L95 ANSWER 28 OF 31 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
 ACCESSION NUMBER: 2003-532852 [50] WPIDS
 DOC. NO. CPI: C2003-144068
 TITLE: Identifying similar surface motifs of **molecular** sequences by identifying surface motifs and subsequences, generating comparison metrics, calculating statistical significance and identifying **molecular** sequences.

DERWENT CLASS: B04 J04
 INVENTOR(S): ADAMIAN, L; BINKOWSKI, T A; LIANG, J; BINKOWSKI, A T
 PATENT ASSIGNEE(S): (ADAM-I) ADAMIAN L; (BINK-I) BINKOWSKI T A; (LIAN-I) LIANG J; (UNII) UNIV ILLINOIS FOUND
 COUNTRY COUNT: 100
 PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG	MAIN	IPC
WO 2003048724	A2	20030612	(200350)*	EN	85	G01N000-00	
RW: AT BE BG CH CY CZ DE DK EA EE ES FI FR GB GH GM GR IE IT KE LS LU							
MC MW MZ NL OA PT SD SE SK SL SZ TR TZ UG ZM ZW							
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK							
DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR							
KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT							
RO RU SD SE SG SI SK SL TJ TM TN TR TT TZ UA UG US UZ VN YU ZA ZM							
ZW							
US 2003149537	A1	20030807	(200358)			G06F019-00	
AU 2002365755	A1	20030617	(200419)			G01N000-00	

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2003048724	A2	WO 2002-US38030	20021127
US 2003149537	A1 Provisional	US 2001-333969P	20011129
	Provisional	US 2001-334689P	20011130
		US 2002-306296	20021127
AU 2002365755	A1	AU 2002-365755	20021127

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 2002365755	A1 Based on	WO 2003048724

PRIORITY APPLN. INFO: US 2001-334689P 20011130; US
 2001-333969P 20011129; US
 2002-306296 20021127

INT. PATENT CLASSIF.:

MAIN: G01N000-00; G06F019-00

BASIC ABSTRACT:

WO2003048724 A UPAB: 20030805

NOVELTY - Identifying similar surface motifs of molecular sequences comprises identifying surface motifs of molecular sequences and sub-sequences having groups of atoms from the molecular sequences associated with surface motifs, generating comparison metrics, calculating statistical significance of at least one comparison metric and identifying molecular sequences similar to the molecular sequences.

USE - Used for identifying similar surface motifs of molecular sequences.

ADVANTAGE - The method takes into account the nature of the surface features and geometric orientation.

DESCRIPTION OF DRAWING(S) - The drawing shows an alternative flow diagram for identifying similar molecular structures.

Dwg.9/9

FILE SEGMENT: CPI
 FIELD AVAILABILITY: AB; GI; DCN
 MANUAL CODES: CPI: B04-C02; B04-C03; B04-E01; B04-E03; B04-N04;
 B11-C08; B11-C08F; B12-K04E; J04-C02

L95 ANSWER 29 OF 31 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
 ACCESSION NUMBER: 2001-201924 [20] WPIDS
 DOC. NO. NON-CPI: N2001-143968
 DOC. NO. CPI: C2001-059902
 TITLE: Classification of molecules, for e.g. assisting
 with the selection of chemical compounds for further
 study, by forming a three-dimensional body representative

of structure of the **molecule**, and generating structural descriptors.

DERWENT CLASS: B04 J04 S03
 INVENTOR(S): EDELSBRUNNER, H; LIANG, J
 PATENT ASSIGNEE(S): (EDEL-I) EDELSBRUNNER H; (LIAN-I) LIANG J
 COUNTRY COUNT: 1
 PATENT INFORMATION:

PATENT NO	KIND DATE	WEEK	LA	PG MAIN IPC
US 6182016	B1 20010130	(200120)*		19 G01N033-50

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
US 6182016	B1	US 1997-918624	19970822

PRIORITY APPLN. INFO: US 1997-918624 19970822

INT. PATENT CLASSIF.:

MAIN: G01N033-50

BASIC ABSTRACT:

US 6182016 B UPAB: 20010410

NOVELTY - Molecules are classified by forming a three-dimensional body representative of structure of the molecule; generating structural descriptors reflecting structural information about neighboring atomic centers or groups of atomic centers of the molecule; and classifying the molecule using the descriptors by identifying values associated with the descriptors.

DETAILED DESCRIPTION - Classification of molecules comprises (i) forming a 3-dimensional body representative of structure of the molecule by placing a potentially overlapping ball around each atom or group of atoms of the molecule; (ii) generating structural descriptors reflecting structural information about neighboring atomic centers or groups of atomic centers of the molecule; and (iii) classifying the molecule using the descriptors by identifying values associated with the descriptors. The ball has a radius for the particular type of atom or group of atoms. The structural descriptors relate to a Voronoi diagram corresponding to the 3-dimensional body.

INDEPENDENT CLAIMS are also included for:

(a) an electronic storage device comprising a storage medium which stores a computer program for implementing the specified classification method;

(b) a method of identifying molecules that are similar to a known compound by classifying the known compound based on the above method, identifying significant elements in the classification method in terms of classification parameters, determining classifications of relevant molecules having the identified classification parameters similar or identical with the known compounds, and establishing the structure of a molecule corresponding to the determined classification of relevant molecules;

(c) a method of evaluating the degree of similarity between two molecules by determining the degree of similarity between the two compounds based on a comparison of the descriptors determined for each molecule; and

(d) a method of selecting and evaluating the efficacy of a chemical compound using a chemical or pharmacological test.

USE - The method is used for assisting with the selection of chemical compounds for further study; for identifying and evaluating similarities and differences between molecules that may be reflected in the behavior of the molecules; and for computing 3-dimensional descriptors useful in

3-dimensional sub-structure searching, similarity searching, combinatorial chemistry, library design, and diversity management. Molecular descriptors are of central importance for developing high throughput screening for drug lead searching and drug lead optimization.

ADVANTAGE - The method provides an accurate and efficient approach for computing 3-dimensional descriptors.

Dwg.0/8

FILE SEGMENT: CPI EPI
FIELD AVAILABILITY: AB
MANUAL CODES: CPI: B11-C08; B12-K04E; J04-B01
EPI: S03-E14H

L95 ANSWER 30 OF 31 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
ACCESSION NUMBER: 2000-039199 [03] WPIDS
DOC. NO. NON-CPI: N2000-029533
TITLE: Three dimensional object surface feature reconstruction
generating system for determining actual 3D shapes and
volumes of objects.
DERWENT CLASS: T01
INVENTOR(S): ALBECK, D; SHASHUA, A
PATENT ASSIGNEE(S): (COGN-N) COGNITENS LTD; (YISS) YISSUM RES & DEV CO
COUNTRY COUNT: 20
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG	MAIN	IPC
WO 9959100	A1	19991118	(200003)*	EN	29	G06K009-00	
RW: AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE							
W: CA JP							
EP 1194881	A1	20020410	(200232)	EN		G06K009-00	
R: DE FR GB							

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 9959100	A1	WO 1999-IB1226	19990514
EP 1194881	A1	EP 1999-950370	19990514
		WO 1999-IB1226	19990514

FILING DETAILS:

PATENT NO	KIND	PATENT NO
EP 1194881	A1 Based on	WO 9959100

PRIORITY APPLN. INFO: US 1998-96359P 19980813; US
1998-85501P 19980514

INT. PATENT CLASSIF.:

MAIN: G06K009-00

BASIC ABSTRACT:

WO 9959100 A UPAB: 20000118

NOVELTY - A post-transformation projective

representation generator is configured to generate post-transformation projective representation in relation to relationships between epipoles in respective image planes for images in each of pre-transformation image set and post-transformation image set.

DETAILED DESCRIPTION - The pre-transformation image set comprise images recorded prior to transformation. The post-transformation image set comprise images recorded subsequent to transformation. An Euclidian representation generator produce Euclidian representation of surface element in scene, using post-transformation projection

and **projective**-to-Euclidian matrix. INDEPENDENT CLAIMS are also included for the following:

(a) 3D object surface feature reconstruction generating method;

(b) 3D object surface feature reconstruction generating program

USE - For determining actual 3D shapes and volumes of objects, and also for computer vision and robotics.

ADVANTAGE - Facilitates reconstruction using images recorded by cameras. **Control points** are available in scene as recorded following non-rigid transformation.

DESCRIPTION OF DRAWING(S) - The figure shows flowchart of Euclidian reconstruction generator.

Dwg.3/4

FILE SEGMENT: EPI
FIELD AVAILABILITY: AB; GI
MANUAL CODES: EPI: T01-J10C4; T01-S02

L95 ANSWER 31 OF 31 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
ACCESSION NUMBER: 1983-B7985K [06] WPIDS
DOC. NO. NON-CPI: N1983-023277
TITLE: Correcting for aberrations in photogrammetric projection
- using four reference marks with automatic metering on
projected plane of aerial photograph.
P82 P83 S02 S06
DERWENT CLASS:
INVENTOR(S): SPATA, P
PATENT ASSIGNEE(S): (JENA) JENOPTIK JENA GMBH; (KOCH-I) KOCH R
COUNTRY COUNT: 4
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG	MAIN	IPC
DE 3214050	A	19830203	(198306)*		7		
DD 200820	A	19830615	(198341)				
US 4482223	A	19841113	(198448)				
CH 656223	A	19860613	(198630)				
DD 200820	B	19870121	(198720)				

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
US 4482223	A	US 1982-388687	19820615

PRIORITY APPLN. INFO: DD 1981-231974 19810722
INT. PATENT CLASSIF.: G01C011-04; G03B023-08; G03B027-68; G03C005-00

BASIC ABSTRACT:

DE 3214050 A UPAB: 19930925

The original aerial photograph (B) is exposed to four reference markings (1,2,3,4) in the four quadrants, before processing. When projected onto a plan (P) the automatic focus control for the lens (O) monitors the fit of the reference markings and provides a best possible fit.

The projector is linked to a processor which ensures that any lens aberration is catered for with the larger magnifications. The system operates automatically and rapidly and compensates for inclination, curvature etc. which would otherwise lead to false perspective.

1/1

FILE SEGMENT: EPI GMPI
FIELD AVAILABILITY: AB
MANUAL CODES: EPI: S02-B04; S06-B04A

=> fil hom

FILE 'HOME' ENTERED AT 12:32:01 ON 23 FEB 2005

=>

This Page Blank (uspto)